

From: Hamud, Fozia  
Sent: Thursday, March 03, 2005 3:29 PM  
To: STIC-Biotech/ChemLib  
Subject: sequence search for 09/617,720

Please search SEQ ID NOs: 1, 2, 3 of 09/617,720 against commercial and interference data bases. thanks.

**Fozia Hamud**  
**Patent Examiner**  
**Remsen 4D64**  
**Mail Box: Remsen 4C70**  
**(571) 272-0884**

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MAR - 3 2005  
STIC-BIOTECH/ChemLib

\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2- \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: 3/14 \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search

NA Sequence: # \_\_\_\_\_  
AA Sequence: # \_\_\_\_\_  
Structure: # \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 13, 2005, 11:56:15 ; Search time 137.39 Seconds

(without alignments)  
11636.250 Million cell updates/sec

Title: US-09-617-720A-3

Perfect score: 42

Sequence: 1 aggaaggaggagaagga.....gagtgaaggaggagtga 42

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_hic: \*  
4: gb\_est3: \*  
5: gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_gss1: \*  
9: gb\_gss2: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	858	BI090567	BI090567 602855674
2	42	100.0	985	AL545100	AL545100 AL545100
3	42	100.0	2605	CR613851	CR613851 full-length
4	34.6	82.4	818	BG787987	BG787987 SEAMC007
C 5	33	78.6	643	AZ649302	AZ649302 IM0518F16
C 6	31.4	74.8	103	AI252833	AI252833 qv49f02.x
C 7	31.4	74.8	154	AZ022385	AZ022385 RPCI-23-3
C 8	31.4	74.8	156	CE100567	CE100567 tigr-gss-
C 9	31.4	74.8	161	AZ714952	AZ714952 RPCI-24-1
C 10	31.4	74.8	170	AQ980187	AQ980187 RPCI-23-3
C 11	31.4	74.8	346	AZ686861	AZ686861 CMT180H20
C 12	31.4	74.8	408	AQ628256	AQ628256 CITBI-EI-
C 13	31.4	74.8	424	AA794173	AA794173 vu67b07.r
C 14	31.4	74.8	514	AA684355	AA684355 vm69d08.r
C 15	31.4	74.8	524	CF898116	CF898116 A0234D08-
C 16	31.4	74.8	554	AZ296671	AZ296671 RPCI-23-1
C 17	31.4	74.8	560	AZ632723	AZ632723 IM0487G01
C 18	31.4	74.8	581	CF897840	CF897840 A0230F01-
C 19	31.4	74.8	585	BG802700	BG802700 0184-18 M
C 20	31.4	74.8	586	AZ709886	AZ709886 RPCI-24-6
C 21	31.4	74.8	609	B0749184	B0749184 UI-M-FD0-
C 22	31.4	74.8	629	CE381159	CE381159 tigr-gss-
C 23	31.4	74.8	653	BI661220	BI661220 603304558
C 24	31.4	74.8	655	CE829872	CE829872 tigr-gss-

25	31.4	74.8	696	8	AZ319198	AZ319198 LM0038M08
26	31.4	74.8	733	8	AZ748464	AZ748464 RPCI-24-1
C 27	31.4	74.8	795	4	BI251681	BI251681 603994176
C 28	31.4	74.8	1163	4	BI664455	BI664455 603290031
C 29	31	73.8	854	8	AQ745575	AQ745575 HS 2272 A
C 30	30.8	73.3	183	6	CB606703	CB606703 AMGNNUC-Y
C 31	30.8	73.3	303	7	H32873	H32873 EST108382 R
C 32	30.8	73.3	330	1	AA736512	AA736512 oad1909.s
C 33	30.8	73.3	346	6	C06764	C06764 C06764 Rat
C 34	30.8	73.3	424	8	BZ263903	BZ263903 CH230-420
C 35	30.8	73.3	435	4	BG667137	BG667137 DRA04G03
C 36	30.8	73.3	457	6	CB740130	CB740130 AMGNNUC-Y
C 37	30.8	73.3	471	2	BF522708	BF522708 UI-R-C0-u
C 38	30.8	73.3	494	1	AI575683	AI575683 UI-R-C0-u
C 39	30.8	73.3	562	8	AZ712287	AZ712287 RPCI-24-1
C 40	30.8	73.3	586	8	BH256925	BH256925 CH230-242
C 41	30.8	73.3	748	8	BZ771226	BZ771226 MGC73F10
C 42	30.8	73.3	750	9	AG281713	AG281713 M18 muscu
C 43	30.8	73.3	825	8	BZ184962	BZ184962 CH230-377
C 44	30.8	73.3	967	8	CC247236	CC247236 CH261-136
C 45	30.8	73.3	1229	9	CL079684	CL079684 CH216-156

## ALIGNMENTS

RESULT 1  
BI090567  
LOCUS 602855674F1 NIH\_MGC\_10 Homo sapiens cDNA clone IMAGE:4996939 5',  
DEFINITION mRNA sequence.  
ACCESSION BI090567  
VERSION BI090567.1 GI:14508897  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 858)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs@mail.nih.gov](mailto:cgapbs@mail.nih.gov)  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Incyte Genomics, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM11023 row: c column: 20  
High quality sequence stop: 670.  
Location/Qualifiers  
source  
1..858  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4996939"  
/cell\_line="MGC36"  
/lab\_host="DH10B"  
/note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.5 kb. Library prepared by Life  
Technologies."

Query Match 100.0%; Score 42; DB 4; Length 858;  
Best Local Similarity 100.0%; Pred. No. 0.046;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAGGAGGAGGAGGAGGAGTGAAGGAGGAGTGAAG 42





**ORIGIN**

Query Match	78.6%	Score 33	DB 8	Length 643
Best Local Similarity	87.8%	Pred. No. 16		
Matches	36	Conservative	0	Mismatches 5; Indels 0; Gaps 0;
QY	2	AGGAGGAGGGAGAGGGAGGAGTGAAGGAGGAGTGA	42	
Db	104	AGGATGGAGTGAAGAGGAGGAGGAGGAGGAGGAGTGA	64	

RESULT 6	
AI252833	LOCUS
AI252833	DEFINITION
AI252833	ACCESSION
AI252833	VERSION
AI252833.1	KEYWORDS
GI:3849362	SOURCE
EST.	ORGANISM
AI252833	Human sapiens (human)
AI252833	Hom sapiens
AI252833	Hom sapiens
AI252833	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AI252833	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AI252833	1 (bases 1 to 103)
AI252833	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .
AI252833	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
AI252833	Tumor Gene Index
AI252833	Unpublished (1997)
AI252833	Contact: Robert Strausberg, Ph.D.
AI252833	Email: <a href="mailto:cgapsb-r@mail.nih.gov">cgapsb-r@mail.nih.gov</a>
AI252833	unknown library type
AI252833	Seq primer: -40UP from Gibco.

```

i.:.103
source
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="IMAGE:1984923"
/sex="female"
/tissue_type="papillary serous carcinoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP_Ov32"
/note="Organ: ovary; Vector: pAMPl; mRNA made from ovarian carcinoma. cDNA made by oligo-dT priming."

```

ORIGIN  
 Query Match 74.8%; Score 31.4; DB 1; Length 103;  
 Best Local Similarity 85.4%; Pred. No. 37;  
 Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 Non-directionally cloned. Size-selected on agarose gel;  
 average insert size 500 bp. Non-amplified library. "

	Query Match	74.8%	Score 31.4	DB 1	Length 103
	Best Local Similarity	85.4%	Pred. No. 37		
	Matches 35	Conservative 0	Mismatches 6	Indels 0	Gaps 0
QY	2	AGGAGGAGGGGAGAGGGGAGGAGTGAAGGAAGGAGTGA	42		
Db	27	AGGAGGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG	67		

RESULT 7	AZ022385	154 bp	DNA	linear	GSS 25-FEB-2000
LOCUS	RP021-23-385H23.TV	RP021-23	Mus musculus	genomic clone	
DEFINITION	RP021-23-385H23, genomic survey sequence.				
ACCESSION	AZ022385				
VERSION	AZ022385.1	GI:7097769			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 154)				
AUTHORS	Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akhmet, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.				

```

TITLE      Mouse BAC End Sequences from Library RPCI-23
JOURNAL    Unpublished (1999)
COMMENT    Other GSSs: RPCI-23-385H23.TU
           Contact: Shaying Zhao
           Department of Eukaryotic Genomics
           The Institute for Genomic Research
           9712 Medical Center Dr., Rockville, MD 20850, USA
           Tel: 301 838 0200
           Fax: 301 838 0208
           Email: szhao@tigr.org
           Clones are derived from the mouse BAC library RPCI-23. For BAC
           library availability, please contact Pieter de Jong
           (pieterdejong.med.buffalo.edu). Clones may be purchased from
           BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
           or from Resea ch Genetics (info@resgen.com). BAC end page:
           http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
           Plate: 385 row: H column: 23
           Seq primer: T7
           Class: BAC ends.
FEATURES   Location/Qualifiers
source     1..156
           /organism="Mus musculus"
           /mol_type="genomic DNA"
           /strain="C57BL/6J"
           /db_xref="taxon:10090"
           /clone="RPCI-23-385H23"
           /sex="Female"
           /lab_host="DH10B"
           /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:
           EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
           brain genomic DNA was isolated and partially digested
           with a combination of EcoRI and EcoRI Methylase. Size
           selected DNA was cloned into the pBACe3.6 vector at the
           EcoRI sites. The ligation products were transformed into
           DH10B electrocompetent cells (BRL Life Technologies)."
ORIGIN
Query Match      74.8%; Score 31.4; DB 8; Length 154;
Best Local Similarity 85.4%; Pred. No. 39;
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1  AAGGAAGGAGGAGGAGGAGGAGTGAAGGAGGAGTGAAGTGA 41
Db 61 AAGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA 21

RESULT 8
CE100567
LOCUS      tigr-gss-dog-17000371107331 Dog Library Canis familiaris genomic,
DEFINITION genomic survey sequence.
ACCESSION CE100567.1 GI:35167452
VERSION    1
KEYWORDS   GSS.
SOURCE     Canis familiaris (dog)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
           1 (bases 1 to 156)
AUTHORS    Kirkness,E.F., Batna,V., Halpern,A.L., Levy,S., Remington,K.,
           Rusch,D.B., Deicher,A.L., Pop,M., Wang,W., Fraser,C.M. and
           Venter,J.C.
           The dog genome: survey sequencing and comparative analysis
TITLE      Science 301 (5641), 1898-1903 (2003)
JOURNAL    22875432
MEDLINE    14512627
COMMENT    Contact: Kirkness EF
           The Institute for Genomic Research
           Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
           Rockville, MD 20850, USA
           Tel: 301-838-0200
           Fax: 301-838-0208

TITLE      Mouse BAC End Sequences from Library RPCI-24
JOURNAL    Unpublished (1999)
COMMENT    Other GSSs: RPCI-24-122O14.TU
           Contact: Shaying Zhao
           Department of Eukaryotic Genomics
           The Institute for Genomic Research
           9712 Medical Center Dr., Rockville, MD 20850, USA
           Tel: 301 838 0200
           Fax: 301 838 0208
           Email: szhao@tigr.org
           Clones are derived from the mouse BAC library RPCI-24. For BAC
           library availability, please contact Pieter de Jong
           (pdejong@mail.cho.org). Clones may be purchased from BACPAC
           Resources (http://www.choi.org/bacpac/orderingframe.htm). BAC end
           page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
           Plate: 122 row: O column: 14
           Seq primer: SP6
           Class: BAC ends.
FEATURES   Location/Qualifiers
source     1..161
           /organism="Mus musculus"
           /mol_type="genomic DNA"
           /strain="C57BL/6J"
           /db_xref="taxon:10090"
           /clone="RPCI-24-122O14"
           /sex="Male"
           /cell_type="Spleen/Brain"
           /clone_lib="RPCI-24"
           /note="Vector: pTARBAC1; Site 1: BamHI; Site 2: BamHI;
           RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
           library was cloned in the pTARBAC1 cloning vector at the
           BamHI sites using MboI partially digested male C57BL/6J
           DNA."
ORIGIN
Query Match      74.8%; Score 31.4; DB 9; Length 156;
Best Local Similarity 85.4%; Pred. No. 39;
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1  AAGGAAGGAGGAGGAGGAGGAGTGAAGGAGGAGTGAAGTGA 41
Db 23 AAGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA 63

RESULT 9
AZ714952/c
LOCUS      RPCI-24-122O14.TU RPCI-24 Mus musculus genomic clone
DEFINITION RPCI-24-122O14, genomic survey sequence.
ACCESSION AZ714952
VERSION    1 GI:12451177
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
           1 (bases 1 to 161)
AUTHORS    Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
           Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
           Russell,D., de Jong,P. and Fraser,C.M.
           Mouse BAC End Sequences from Library RPCI-24
           Unpublished (1999)
           Other GSSs: RPCI-24-122O14.TV
           Contact: Shaying Zhao
           Department of Eukaryotic Genomics
           The Institute for Genomic Research
           9712 Medical Center Dr., Rockville, MD 20850, USA
           Tel: 301 838 0200
           Fax: 301 838 0208
           Email: szhao@tigr.org
           Clones are derived from the mouse BAC library RPCI-24. For BAC
           library availability, please contact Pieter de Jong
           (pdejong@mail.cho.org). Clones may be purchased from BACPAC
           Resources (http://www.choi.org/bacpac/orderingframe.htm). BAC end
           page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
           Plate: 122 row: O column: 14
           Seq primer: SP6
           Class: BAC ends.
FEATURES   Location/Qualifiers
source     1..161
           /organism="Mus musculus"
           /mol_type="genomic DNA"
           /strain="C57BL/6J"
           /db_xref="taxon:10090"
           /clone="RPCI-24-122O14"
           /sex="Male"
           /cell_type="Spleen/Brain"
           /clone_lib="RPCI-24"
           /note="Vector: pTARBAC1; Site 1: BamHI; Site 2: BamHI;
           RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
           library was cloned in the pTARBAC1 cloning vector at the
           BamHI sites using MboI partially digested male C57BL/6J
           DNA."
ORIGIN

```

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Query Match      74.8%; Score 31.4; DB 8; Length 161;
Best Local Similarity 85.4%; Pred. No. 39;
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AAGGAGGAGGAGGAGGAGGAGGAGTGAAGGAGGAGTGA 41
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 102 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATGAA 62

RESULT 10
LOCUS      AQ980187/c
DEFINITION RPCI-23-342A9.TV RPCI-23 Mus musculus genomic clone RPCI-23-342A9,
Genomic survey sequence.
ACCESSION  AQ980187
VERSION     AQ980187.1 GI:6812488
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus

REFERENCE
AUTHORS    Zhao,S., Nieman,W., Feldblyum,T., Malek,J., Shatsman,S.,
Akinret,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de
Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other GSSs: RPCI-23-342A9.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pietere@jeng.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac/ends/mouse/bac_end_intro.html
Plate: 342 row: A column: 9
Seq primer: T7
Class: BAC ends.

FEATURES
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Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-342A9"
/sex="female"
/lab_host="DH10B"
/clone_lib="RPCI-23"
/notes="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methyase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."

ORIGIN
Query Match      74.8%; Score 31.4; DB 8; Length 170;
Best Local Similarity 85.4%; Pred. No. 39;
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AAGGAGGAGGAGGAGGAGGAGGAGTGAAGGAGGAGTGA 41
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 106 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA 66

RESULT 11

Query Match      74.8%; Score 31.4; DB 8; Length 346;
Best Local Similarity 85.4%; Pred. No. 43;
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AAGGAGGAGGAGGAGGAGGAGGAGTGAAGGAGGAGTGA 41
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 344 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA 304

RESULT 12

Query Match      74.8%; Score 31.4; DB 8; Length 346;
Best Local Similarity 85.4%; Pred. No. 43;
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AAGGAGGAGGAGGAGGAGGAGGAGTGAAGGAGGAGTGA 41
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 344 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA 304

RESULT 13/c
LOCUS      AZ868613
DEFINITION 2M0180H20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0180H20 F, genomic survey sequence.
ACCESSION  AZ868613
VERSION     AZ868613.1 GI:13072103
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus

REFERENCE
AUTHORS    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0180 row: H column: 20
Seq primer: CGTTGTAAACGACGAGCCAGT
Class: plasmid ends
High quality sequence stop: 346.

FEATURES
source
Location/Qualifiers
1..346
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0180H20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match      74.8%; Score 31.4; DB 8; Length 346;
Best Local Similarity 85.4%; Pred. No. 43;
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AAGGAGGAGGAGGAGGAGGAGTGAAGGAGGAGTGA 41
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 344 AAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA 304

```



Research Program, NIH (<http://lgsum.grc.nia.nih.gov/cDNA>). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001)). [PMID: 11544199]]. EG cells were obtained from Dr. Brigid L.M. Hogan and RNA was prepared by Dr. Mark G. Carter (NIH/NIA-IRP). EG cells were cultured at 37 °C, 5% CO<sub>2</sub> in DMEM supplemented with 15% ES cell-qualified FBS, 0.1mM non-essential amino acids, 2 mM glutamine, penicillin/streptomycin, 1 mM sodium pyruvate, 0.1 mM beta-mercaptoethanol, and 10<sup>-7</sup> units of LiF per liter. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [(Invitrogen: 5'-pGACTAGTTCTACATCGAGCGGCCCTTTTTTTTTT-3')] from 2.5 µg of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were double digested with NotI and SalI enzymes, then purified by phenol/chloroform and Centricon 100. The cDNA mixture was subjected to a special subtraction procedure by Dr. Kazuhiro Kondo at AINIS Cosmos. Then the subtracted cDNAs were cloned into SalI/NotI site of pCWV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.2kb. The library was constructed by Yulan Piao and Kazuhiro Kondo."

ORIGIN

	Query Match	74.8%;	Score 31.4;	DB 7;	Length 524;
	Best Local Similarity	85.4%;	Pred. No. 45;		
	Matches	35;	Mismatches	6;	Indels 0; Gaps 0;
Qy	1	AAGGAAGGAGGGAGAAGGAGGAGTGTAAGGAAGGAGGTCAA 41 			
Db	447	AAGGAAGGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGAA 407 			

Search completed: March 13, 2005, 18:14:03  
Job time : 144.39 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 13, 2005, 12:28:28 ; Search time 478.866 Seconds  
(without alignments)  
8757.724 Million cell updates/sec

Title: US-09-617-720A-1

Perfect score: 2563

Sequence: 1 agggaggtctacacctgtg.....ataatatcgagagaagaga 2563

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents: NA.\*

1: /cgn2\_6/prodata/1/ina/5A COMB.seq.\*

2: /cgn2\_6/prodata/1/ina/5B COMB.seq.\*

3: /cgn2\_6/prodata/1/ina/6A COMB.seq.\*

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5: /cgn2\_6/prodata/1/ina/PCUS COMB.seq.\*

6: /cgn2\_6/prodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2515.2	98.1	2699	4	US-09-949-016-3485
2	2488.4	97.1	2648	3	US-09-417-455-6
3	2488.4	97.1	2648	3	US-09-348-942-6
4	2488.4	97.1	2648	3	US-09-457-626-6
5	2488.4	97.1	2648	4	US-09-576-008-6
6	2488.4	97.1	2720	4	US-09-949-016-956
7	2245.2	87.6	9634	4	US-09-949-016-12698
8	2245.2	87.6	9641	4	US-09-949-016-15227
9	2220.4	86.6	7605	3	US-09-417-455-8
10	2220.4	86.6	7605	3	US-09-348-942-8
11	2220.4	86.6	7605	3	US-09-457-626-8
12	2220.4	86.6	7605	4	US-09-576-008-8
13	1616.6	63.1	5751	3	US-09-417-455-7
14	1616.6	63.1	5751	3	US-09-348-942-7
15	1616.6	63.1	5751	3	US-09-457-626-7
16	1616.6	63.1	5751	4	US-09-576-008-7
17	1195.2	46.6	1282	3	US-09-417-455-4
18	1195.2	46.6	1282	3	US-09-348-942-4
19	1195.2	46.6	1282	3	US-09-457-626-4
20	1195.2	46.6	1282	4	US-09-576-008-4
21	941.2	36.7	985	3	US-09-417-455-2
22	941.2	36.7	985	3	US-09-348-942-2
23	941.2	36.7	985	3	US-09-457-626-2
24	941.2	36.7	985	4	US-09-576-008-2
25	600.6	23.4	601	4	US-09-949-016-36664
26	600.6	23.4	601	4	US-09-949-016-123784
27	285	11.1	357	3	US-09-417-455-1

28	285	11.1	357	3	US-09-348-942-1	Sequence 1, Appli	
29	285	11.1	357	3	US-09-457-626-1	Sequence 1, Appli	
30	285	11.1	357	4	US-09-576-008-1	Sequence 1, Appli	
31	198.6	7.7	466	4	US-09-573-080A-102	Sequence 102, App	
C	32	155.8	6.1	374159	4	US-09-949-016-15868	Sequence 15868, A
33	153.2	6.0	100550	4	US-09-949-016-11835	Sequence 11835, A	
34	153.2	6.0	100551	4	US-09-949-016-16207	Sequence 16207, A	
35	149.2	5.8	95750	4	US-09-949-016-11926	Sequence 11926, A	
C	36	149.2	5.8	213456	4	US-09-820-007-3	Sequence 3, Appli
C	37	149.2	5.8	323820	4	US-09-949-016-14139	Sequence 14139, A
38	148.4	5.8	231129	4	US-09-949-016-16110	Sequence 16110, A	
39	148.4	5.8	266293	4	US-09-949-016-11934	Sequence 11934, A	
40	145.4	5.7	124480	4	US-09-949-016-15921	Sequence 15921, A	
C	41	139.2	5.4	64046	4	US-09-949-016-12560	Sequence 12560, A
C	42	139.2	5.4	64047	4	US-09-949-016-15781	Sequence 15781, A
C	43	139	5.4	60417	4	US-09-949-016-13312	Sequence 13312, A
C	44	138.8	5.4	390890	4	US-09-949-016-14720	Sequence 14720, A
C	45	138.6	5.4	108310	4	US-09-949-016-16366	Sequence 16366, A

#### ALIGNMENTS

RESULT 1

US-09-949-016-3485

; Sequence 3485, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3485

; LENGTH: 2699

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-3485

Query Match 98.1%; Score 2515.2; DB 4; Length 2699;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 2553; Conservative 0; Mismatches 8; Indels 3; Gaps 3;

QY 1 AGGGAGTCTACACCTGTGGAGCTCAAGATGGTCTGAGTGGGGCGCTGTGCTTCGAA 60

DB 133 AGGGAGTCTACACCTGTGGAGCTCAAGATGGTCTGAGTGGGGCGCTGTGCTTCGAA 192

QY 61 TGAAGGACTCGGCATTGAAGGTCTTTATCTGCATAATAACCACTTCTAGCTGGAGGC 120

DB 193 TGAAGGACTCGGCATTGAAGGTCTTTATCTGCATAATAACCACTTCTAGCTGGAGGC 252

QY 121 TGCATGCAGGAAGGTCAATTAAGGTGAAGAGATCAAGCTGGTCCCAATCGGTGGCTGG 180

DB 253 TGCATGCAGGAAGGTCAATTAAGGTGAAGAGATCAAGCTGGTCCCAATCGGTGGCTGG 312

QY 181 ATGCCAGCTGTCCCGCTCATCTGGGTGTCAGGTTGGAAGCCAGTGCCTCTCATGTG 240

DB 313 ATGCCAGCTGTCCCGCTCATCTGGGTGTCAGGTTGGAAGCCAGTGCCTCTCATGTG 372

QY 241 GGGTGGGAGAGCCGAGTCTTAACACTAGACCACTGAGCCAGTGAACATGAGCTTATCTTG 300

DB 373 GGGTGGGAGAGCCGAGTCTTAACACTAGACCACTGAGCCAGTGAACATGAGCTTATCTTG 432

QY 301 GTGCCAAGGAATCCAAAGAGCTTCACTTCTACCGGGGGGACATGGGGCTCACCTCCAGCT 360

Db 433 GTGCCAAGAAATCCAGAGCTTACCTTCTACGGGGGACATGGGGCTCACCTCCAGCT 492  
QY 361 TCGAGTCGGCTGCTACCCGGGCTGGTCTCTGTGACGGTGCTGTAAGCCGATCAGCCTG 420  
Db 493 TCGAGTCGGCTGCTACCCGGGCTGGTCTCTGTGACGGTGCTGTAAGCCGATCAGCCTG 552  
QY 421 TCAGACTCACCCAGCTTCCCGAAGATGGTGGTGGAAATGCCCCCATCAAGACTTCTACT 480  
Db 553 TCAGACTCACCCAGCTTCCCGAAGATGGTGGTGGAAATGCCCCCATCAAGACTTCTACT 612  
QY 481 TCAGAGCTGTGACTAGGGCAAGTGCCTCCCGAGAACTCTCTGGGACAGAGCCAGCTGG 540  
Db 613 TCAGAGCTGTGACTAGGGCAAGTGCCTCCCGAGAACTCTCTGGGACAGAGCCAGCTGG 671  
QY 541 GTGAGGGTGTGAGGAGAGCCATGGGGGACAACTCTCTGGTTCAGAGCCGCC 600  
Db 672 GTGAGGGTGTGAGGAGAGCCATGGGGGACAACTCTCTGGTTCAGAGCCGCC 731  
QY 601 CAGGTCTGACTTGTGGGACCTGACCACTTGTCTCTGGTTCAGAGTTCATATAAT 660  
Db 732 CAGGTCTGACTTGTGGGACCTGACCACTTGTCTCTGGTTCAGAGTTCATATAAT 791  
QY 661 CTGAGATTTGAGCTCAGTCAGGCTCTCCCGCACTGGATGGTGTCTCTGTGGAACT 720  
Db 792 CTGAGATTTGAGCTCAGTCAGGCTCTCCCGCACTGGATGGTGTCTCTGTGGAACT 851  
QY 721 CTGTGAAAACCATGTGGGTAACTGGGAATAACATGAAAGATTTCTGTGGGGTGG 780  
Db 852 CTGTGAAAACCATGTGGGTAACTGGGAATAACATGAAAGATTTCTGTGGGGTGG 911  
QY 781 GTGGGGAGTGTGGGAATCAATCTCTGCTTAATGTGTAACATGCAAGTGTACCTGAGCC 840  
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QY 841 CGCAGGGCAACCCATCCCACTGAGCTTATAGGGTCACTAGCTCTCCACATGAAGTC 900  
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Db 1032 CTGTCACTCACCACCTGTGAGGAGGGAGTGTCTATAGCTCAGGATCTATGGCCCT 1091  
QY 961 TGGCCAGGCCCAACCCCTTCCCTT - ATCTGCGCACTGCTCATATGCTACCTTCTATC 1019  
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QY 1020 TCTTCCCTCATCATCTTGTGTGGGATGAGGAGTGTGATGTCAGAAAGAAATGGTTCG 1079  
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QY 1080 AGCTCAGAGATATAAGATAAGTATAGGTATGCTATCTCTTTTAAACCCCAAGATACA 1139  
Db 1212 AGCTCAGAGATATAAGATAAGTATAGGTATGCTATCTCTTTTAAACCCCAAGATACA 1271  
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Db 1272 ATCAAAATCCAGATGCTGCTCTATTCCTCATGAAAAGTGTCTCATGACATATTGAGAA 1331  
QY 1200 GACCTACTTACAAAGTGGCATATTTGCAATTTATTTTAAATTAAGATACCTATTTATA 1259  
Db 1332 GACCTACTTACAAAGTGGCATATTTGCAATTTATTTTAAATTAAGATACCTATTTATA 1391  
QY 1260 TATTTCTTTATAGAAAAGTCTGAGAGTGTACTTCAATTTGACCAATGTGAGGTTG 1319  
Db 1392 TATTTCTTTATAGAAAAGTCTGAGAGTGTACTTCAATTTGACCAATGTGAGGTTG 1451  
QY 1320 TGGCAGTATAGGTGATTTTCTTTTAAATTTCTGTTAAATTTATCTGTTAAATTTTCT 1379  
Db 1452 TGGCAGTATAGGTGATTTTCTTTTAAATTTCTGTTAAATTTATCTGTTAAATTTTCT 1511  
QY 1380 TCAATGAAGATGAATTCCTTGTATATAAATAAGAAAGAAATTAATCTGTAGGTAAGCA 1439

Db 1512 TCAATGAAGATGAATTCCTTGTATATAAATAAGAAAGAAATTAATCTGTAGGTAAGCA 1571  
QY 1440 GAGCAGACATCATCTCTGATTTCTCTCAGCTCCAAATCCCGAGAGTAAATCAAAATGA 1499  
Db 1572 GAGCAGACATCATCTCTGATTTCTCTCAGCTCCAAATCCCGAGAGTAAATCAAAATGA 1631  
QY 1500 ATCGAGCTCTGCTGCTCTGCTGTTGTAGTATGATCAGGAAACAGATCTCAGCAAGC 1559  
Db 1632 ATCGAGCTCTGCTGCTCTGCTGTTGTAGTATGATCAGGAAACAGATCTCAGCAAGC 1691  
QY 1560 CACTCAGAGGAGGCTGCTGAGTTTGTGGTGGAACTCTCTGGTAAAGAACTTAA 1619  
Db 1692 CACTCAGAGGAGGCTGCTGAGTTTGTGGTGGAACTCTCTGGTAAAGAACTTAA 1751  
QY 1620 GAAACAAATCATCTGGTAAATCTTCTAGAAAGATCACAGCCCTCGGATTCAGAGC 1679  
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QY 1680 ATTGGATCCAGTCTCTAAGAGGCTGTGATCTGTTGAAATGTCTCCCTCAAAATCA 1739  
Db 1812 ATTGGATCCAGTCTCTAAGAGGCTGTGATCTGTTGAAATGTCTCCCTCAAAATCA 1871  
QY 1740 CATCTCTTGGAACTCTCAGTCTGAGTTTATTTGGAGATAAGTCTCTGAGATGTAG 1799  
Db 1872 CATCTCTTGGAACTCTCAGTCTGAGTTTATTTGGAGATAAGTCTCTGAGATGTAG 1931  
QY 1800 TTAGTTAAGACAAAGTCTGCTGATGAAGGTAGACCTAAATTCATATGACTGGTTTCC 1859  
Db 1932 TTAGTTAAGACAAAGTCTGCTGATGAAGGTAGACCTAAATTCATATGACTGGTTTCC 1991  
QY 1860 TTGTATGAAAAGGAGGACACAGAGACAGAGGAGACGCGGGAAAGATATGTAAGATG 1919  
Db 1992 TTGTATGAAAAGGAGGACACAGAGACAGAGGAGACGCGGGAAAGATATGTAAGATG 2051  
QY 1920 AAGCAGAGATCGGAGTTTTCAGCCCAAGCTAAGAAACACCAAGGATTTGGCAACCA 1979  
Db 2052 AAGCAGAGATCGGAGTTTTCAGCCCAAGCTAAGAAACACCAAGGATTTGGCAACCA 2111  
QY 1980 TCAGAAAGCTTGAAGAGGCAAGAAATTTCTTCCCTAGAGGCTTTAGAGGATTAACGCG 2039  
Db 2112 TCAGAAAGCTTGAAGAGGCAAGAAATTTCTTCCCTAGAGGCTTTAGAGGATTAACGCG 2171  
QY 2040 TCTGCTGAAACCTTAATCTCAGACTTCCAGCTCTCTGAAACGAAAGAAATTAATTTCCG 2099  
Db 2172 TCTGCTGAAACCTTAATCTCAGACTTCCAGCTCTCTGAAACGAAAGAAATTAATTTCCG 2231  
QY 2100 CTGTTTAAAGCCCAAGGATTAATTTGTTTACAGAGCTCTAGGAACTAATACAGCTCT 2159  
Db 2232 CTGTTTAAAGCCCAAGGATTAATTTGTTTACAGAGCTCTAGGAACTAATACAGCTCT 2291  
QY 2160 AAAATGATCCCTGTCTCTCGTGTGTTTACATCTGTGTGTCTCCCTCCCAATGTACCA 2219  
Db 2292 AAAATGATCCCTGTCTCTCGTGTGTTTACATCTGTGTGTCTCCCTCCCAATGTACCA 2351  
QY 2220 AAGTTGTCTTTGTGACCAATAGAAATATGGCAGAAAGTGTGATGCGATGCCATTTCCAGAT 2279  
Db 2352 AAGTTGTCTTTGTGACCAATAGAAATATGGCAGAAAGTGTGATGCGATGCCATTTCCAGAT 2410  
QY 2280 AGGTTATAAAGACACTGAGCTTCTACTTGAAGCTCTCTCTGCGCAACCCAGCCGCC 2339  
Db 2411 AGGTTATAAAGACACTGAGCTTCTACTTGAAGCTCTCTCTGCGCAACCCAGCCGCC 2470  
QY 2340 CAATCTATCTTGGCTCACTCGCTCTGGGGAGGCTAGCTGCCATGCTATGAGCAGGCTA 2399  
Db 2471 CAATCTATCTTGGCTCACTCGCTCTGGGGAGGCTAGCTGCCATGCTATGAGCAGGCTA 2530  
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Db 2531 TAAAGAGACTTACGTGGTAAATAAATGAAGTCTCTGCGCAACAGCCACATTAAGTAACTTA 2590  
QY 2460 GAAAGCAGAGACTCTGTGAGATTAATCGATGTTGTTTAAAGTGTCTCAGTTTGGTCT 2519  
Db 2591 GAAAGCAGAGACTCTGTGAGATTAATCGATGTTGTTTAAAGTGTCTCAGTTTGGTCT 2650



QY 2520 AACCTGTTATGAGCAATAGATAAATAATATGAGAGAAAGAGA 2563  
DB 2651 AACCTGTTATGAGCAATAGATAAATAATATGAGAGAAAGAGA 2694

## RESULT 2

US-09-417-455-6  
; Sequence 6, Application US/09417455  
; Patent No. 6294655  
; GENERAL INFORMATION:  
; APPLICANT: Ford, John  
; APPLICANT: Pace, Ann  
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF  
; FILE REFERENCE: 28110/36328  
; CURRENT APPLICATION NUMBER: US/09/417,455  
; CURRENT FILING DATE: 1999-10-13  
; PRIOR APPLICATION NUMBER: US 09/348,942  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: PCT/US99/04291  
; PRIOR FILING DATE: 1999-04-05  
; PRIOR APPLICATION NUMBER: US 09/287,210  
; PRIOR FILING DATE: 1999-04-05  
; PRIOR APPLICATION NUMBER: US 09/251,370  
; PRIOR FILING DATE: 1999-02-17  
; PRIOR APPLICATION NUMBER: US 09/229,591  
; PRIOR FILING DATE: 1999-01-13  
; PRIOR APPLICATION NUMBER: US 09/127,698  
; PRIOR FILING DATE: 1998-07-31  
; PRIOR APPLICATION NUMBER: US 09/099,818  
; PRIOR FILING DATE: 1998-06-19  
; PRIOR APPLICATION NUMBER: US 09/082,364  
; PRIOR FILING DATE: 1998-05-20  
; PRIOR APPLICATION NUMBER: US 09/079,909  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: US 09/055,010  
; PRIOR FILING DATE: 1998-04-03  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 2648  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-417-455-6

Query Match 97.1%; Score 2488.4; DB 3; Length 2648;  
Best Local Similarity 95.4%; Pred. No. 0;  
Matches 2550; Conservative 0; Mismatches 11; Indels 5; Gaps 5;

QY 1 AGGGGAGTCTACACCCCTGTGGAGCTCAAGATGGTCTGAGTGGGGCGCTGTGCTTCCGAA 60  
DB 33 AGGGGAGTCTACACCCCTGTGGAGCTCAAGATGGTCTGAGTGGGGCGCTGTGCTTCCGAA 92  
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DB 93 TGAAGACTCGGCATGGAAGTGTCTTATCTGCATTAATACCAAGCTTCTAGCTGGAGGC 152  
QY 121 TCCATGACGGGAAGTGCATTAAAGGTGAAGAGATCAGCGTGTGCCCAATCGTGGCTGG 180  
DB 153 TGCATGACGGGAAGTGCATTAAAGGTGAAGAGATCAGCGTGTGCCCAATCGTGGCTGG 212  
QY 181 ATGCCAGCTGTCCCGCTCATCTGGGTGTCCAGGGTGGAAAGCCAGTGCCTGTGATGTG 240  
DB 213 ATGCCAGCTGTCCCGCTCATCTGGGTGTCCAGGGTGGAAAGCCAGTGCCTGTGATGTG 272  
QY 241 GGGTGGGAGAGCGGAGCTTAACACATAGAGCAGTGAACATCATGAGAGCTCTATCTTG 300  
DB 273 GGGTGGGAGAGCGGAGCTTAACACATAGAGCAGTGAACATCATGAGAGCTCTATCTTG 332  
QY 301 GTGCCAAGGAATCCAAAGCTTCCACCTTACCGGGGAGCATGGGGCTCACCTCCAGCT 360  
DB 333 GTGCCAAGGAATCCAAAGCTTCCACCTTACCGGGGAGCATGGGGCTCACCTCCAGCT 392

QY 361 TCGAGTCGGCTGCCCTACCCGGGCTGGTTCCTGTGCA CGGTGCTGAAGCGGATCAGCCTG 420  
DB 393 TCGAGTCGGCTGCCCTACCCGGGCTGGTTCCTGTGCA CGGTGCTGAAGCGGATCAGCCTG 452  
QY 421 TCAGACTCACCCAGCTTCCCGAGAAATGGTGGTGGAAATGCCCCATCAGAGCTTCTACT 480  
DB 453 TCAGACTCACCCAGCTTCCCGAGAAATGGTGGTGGAAATGCCCCATCAGAGCTTCTACT 512  
QY 481 TCCAGCAGTGTGACTAGGGCAACGTGCCCCCGAGAACTCCCTGGGAGAGCCAGCTCGG 540  
DB 513 TCCAGCAGTGTGACTAGGGCAACGTG - CCCCCAGAACTCCCTGGGAGAGCCAGCTCGG 571  
QY 541 GTGAGGGTGTGAGTGAGGAGAGACCCATGGCGGCAATCACTCTTCTGCTCTCAGGACCCC 600  
DB 572 GTGAGGGTGTGAGTGAGGAGAGACCCATGGCGGCAATCACTCTCTCTCTCAGGACCCC 631  
QY 601 CAGGTCTGACTTAGTGGGCACCTGACCACTTGTGCTCTTCTGGTTCAGGATTAAT 660  
DB 632 CAGGTCTGACTTAGTGGGCACCTGACCACTTGTGCTCTTCTGGTTCAGGATTAAT 691  
QY 661 CTGAGATTTGGAGCTCAGTCCAGGGTCTCTCCCGCACTGGATGGTGTCTGTCTGAGAAC 720  
DB 692 CTGAGATTTGGAGCTCAGTCCAGGGTCTCTCCCGCACTGGATGGTGTCTGTCTGAGAAC 751  
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DB 752 CTTGTAAAAACCATGTGGGTAAACTGGGAATAACATGAAGAAATTTCTGTGGGGTGG 811  
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DB 812 GTGGGGGAGTGTGGGAATCACTTCTGCTTAATGTAACATGACAACTGTACCTCAGGCC 871  
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DB 872 CGCAGGGCAACCCATCCCGAGTTGAGGCTTATAGGGTCAGTAGCTCTCCACATGAAGTC 931  
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QY 961 TGGCCCGAGCCCGCCCTTCCCTTT - ATCTGCCACTGTCTATGCTACCTTTCTCTATC 1019  
DB 992 TGGCCCGAGCCCGCCCTTCCCTTTAACTCTGCCACTGTCTATGCTACCTTTCTCTATC 1051  
QY 1020 TCTTCCCTCATCATCTTGTGTGGGCATGAGGAGTGGTGTGATGTGACAGAAATGTTCTG 1079  
DB 1052 TCTTCCCTCATCATCTTGTGTGGGCATGAGGAGTGGTGTGATGTGACAGAAATGTTCTG 1111  
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DB 1112 AGCTCAGAAAGATAAAGATAAGTAGGGTATGCTGATCCTCTTTAAAAACCCCAAGATACA 1171  
QY 1140 ATCAAAATCCAGAGTGTGCTCTATTTCCCATGAAAGTGTCTCATGACATATTGAGAA 1199  
DB 1172 ATCAAAATCCAGAGTGTGCTCTATTTCCCATGAAAGTGTCTCATGACATATTGAGAA 1231  
QY 1200 GACCTACTTACAAAGTGGCATATA - TTGCAATTTTATTTTAAATTAAGATACCTATTAT 1258  
DB 1232 GACCTACTTACAAAGTGGCATATA TTGCAATTTTATTTTAAATTAAGATACCTATTAT 1291  
QY 1259 ATATTCTTTATAGAAAAAAGTCTGGAAGATTTACTTCAATGTAGCAATGTGAGGGTG 1318  
DB 1292 ATATTCTTTATAGAAAAAAGTCTGGAAGATTTACTTCAATGTAGCAATGTGAGGGTG 1351  
QY 1319 GTGSCAGTATAGTGTGATTTTCTTTTAAATTTCTGTTTATCTGTTTCTTAATTTT 1378  
DB 1352 GTGSCAGTATAGTGTGATTTTCTTTTAAATTTCTGTTTATCTGTTTCTTAATTTT 1411  
QY 1379 CTACAATGAAGATGAATTTCTTTGTATAAAAATAAGAAAAAATAATCTTGTAGGTGAAG 1438  
DB 1412 CTACAATGAAGATGAATTTCTTTGTATAAAAATAAGAAAAAATAATCTTGTAGGTGAAG 1471  
QY 1439 AGAGCAGACATCATCTCTGATTTGTCTCAGCCTCCAATTTCCCGAGAGTAAATTCAAATTTG 1498



Db 453 TCAGACTACCCAGCTTCCGAGAATGTTGGCTGGAAATGCCCCATCATCAGACTTCTACT 512  
Qy 481 TCCAGAGCTGTGACTAGGCAACGTCGCCCCGAGAACTCCCTGGGCGAGCCAGCTCGG 540  
Db 513 TCCAGCAGTGTGACTAGGGCAACGTC - CCCCCAGAACTCCCTGGGCGAGCCAGCTCGG 571  
Qy 541 GTGAGGGGTGAGTGGAGGAGACCAATGGCGGCAATCACTCTTCTGCTCTCAGGACCCC 600  
Db 572 GTGAGGGGTGAGTGGAGGAGACCCATGGCGGCAATCACTCTCTGCTCTCAGGACCCC 631  
Qy 601 CAGGCTGACTTGTAGTGGGCACTGACCACTTGTCTCTTCTGTTCCAGTTCGATATAAT 660  
Db 632 CAGCTGACTTGTAGTGGGCACTGACCACTTGTCTCTTCTGTTCCAGGTTTGGATAAAT 691  
Qy 661 CTGAGATTGGAGCTCAGTCAGGGTCTCCGCCACTGGATGGTCTACTGCTGTGGAAC 720  
Db 692 CTGAGATTGGAGCTCAGTCAGGGTCTCCGCCACTGGATGGTCTACTGCTGTGGAAC 751  
Qy 721 CTGTGAAAAACCATGTGGGGTAACTGGGAAATAACATGAAGAATTTCTGTGGGGTGGG 780  
Db 752 CTGTGAAAAACCATGTGGGGTAACTGGGAAATAACATGAAGAATTTCTGTGGGGTGGG 811  
Qy 781 GTGGGGGAGTGTGGGAATCATTTCTGCTTAATGGTAACTGCAAGTGTTCACCTGAGCC 840  
Db 812 GTGGGGGAGTGTGGGAATCATTTCTGCTTAATGGTAACTGCAAGTGTTCACCTGAGCC 871  
Qy 841 CCGCAGGCCAAACCATCCCCAGTTGAGCCCTTAAGGGTCAGTGTCTCCACATGAAGTC 900  
Db 872 CCGCAGGCCAAACCATCCCCAGTTGAGCCCTTAAGGGTCAGTGTCTCCACATGAAGTC 931  
Qy 901 CTTCTCACTCACCATGTGCAGAGAGGGAGGTGTCATAGATCAGGGATCTATGCCCT 960  
Db 932 CTGTCACTCACCATGTGCAGAGAGGGAGGTGTCATAGATCAGGGATCTATGCCCT 991  
Qy 961 TGGCCCGAGCCCAACCCCTTCCCTTT - ATCTGCGCACTGTCATATGCTACCTTTCTATC 1019  
Db 992 TGGCCCGAGCCCAACCCCTTCCCTTTAATCTCTGCACTGTGATATGCTACCTTTCTATC 1051  
Qy 1020 TCTTCCCTCATCATTTGTGTGGGATGAGAGGTGGTGTGTCAGAGAAATAGTTTCG 1079  
Db 1052 TCTTCCCTCATCATTTGTGTGGGATGAGAGGTGGTGTGTCAGAGAAATAGTTTCG 1111  
Qy 1080 AGCTCAGAGATAAAGATAAGTAGGGTATGCTGATCCTTTTAAACCACCAAGATACA 1139  
Db 1112 AGCTCAGAGATAAAGATAAGTAGGGTATGCTGATCCTTTTAAACCACCAAGATACA 1171  
Qy 1140 ATCAAAATCCAGATGCTGCTCTATTCCTCATGAAAAGTCTCATGACATATTGAGAA 1199  
Db 1172 ATCAAAATCCAGATGCTGCTCTATTCCTCATGAAAAGTCTCATGACATATTGAGAA 1231  
Qy 1200 GACCTACTTACAAAGTGGCATATA - TTGCAATTTTATTTTAAATAAAGATACCTATTAT 1258  
Db 1232 GACCTACTTACAAAGTGGCATATAATTGCAATTAATTTTAAATAAAGATACCTATTAT 1291  
Qy 1259 ATATTTCTTTATAGAAAAAGTCTGGAAGTTTACTTCAATTTGAGCAATGTCAGGGTG 1318  
Db 1292 ATATTTCTTTATAGAAAAAGTCTGGAAGTTTACTTCAATTTGAGCAATGTCAGGGTG 1351  
Qy 1319 GTGGCAGTATAGTTCATTTTCTTTTAAATTCGTTTAAATTTATCTGATTTTCTTAATTTT 1378  
Db 1352 GTGGCAGTATAGTTCATTTTCTTTTAAATTCGTTTAAATTTATCTGATTTTCTTAATTTT 1411  
Qy 1379 CTACAATGAAGATGAATTTCTTTGTATAAAAAATAAGAAAGAAATTAATCTTGAGGTAAGC 1438  
Db 1412 CTACAATGAAGATGAATTTCTTTGTATAAAAAATAAGAAAGAAATTAATCTTGAGGTAAGC 1471  
Qy 1439 AGAGCAGACATCATCTCGATTGTCCTCGCTCCAAATTTCCCGCAGTAAATTCAAAATTG 1498  
Db 1472 AGAGCAGACATCATCTCGATTGTCCTCGCTCCAAATTTCCCGCAGTAAATTCAAAATTG 1531  
Qy 1499 AATCGAGCTCTGCTGCTGCTGTTGTTGTAGTAGTATCAGGAAACAGATCTCAGCAAG 1558  
Db 1532 AATCGAGCTCTGCTGCTGCTGTTGTTGTAGTAGTATCAGGAAACAGATCTCAGCAAG 1591

RESULT 4

US-09-457-626-6

; Sequence 6, Application US/09457626

Qy 1559 CCACTGAGGAGGAGGCTGTGCTGAGTTTGTGTGGCTGGAAATCTCTGGGTAAAGAACTTAA 1618  
Db 1592 CCACTGAGGAGGAGGCTGTGCTGAAGTTTGTGTGGCTGGAAATCTCTGGGTAAAGAACTTAA 1651  
Qy 1619 AGAAACAAAATCATCTGGTAAATTTCTTCTAGAAAGATCACAGCCCTCGGATTTCCAAGG 1678  
Db 1652 AGAAACAAAATCATCTGGTAAATTTCTTCTAGAAAGATCACAGCCCTCGGATTTCCAAGG 1711  
Qy 1679 CAATGGATCCAGTCTCTAAAGAGGCTGTGTACTGTGTTGAAATTTGTGTCGCCCTCAAAATTC 1738  
Db 1712 CAATGGATCCAGTCTCTAAAGAGGCTGTGTACTGTGTGAATTTGTGTCGCCCTCAAAATTC 1771  
Qy 1739 ACATCTCTTCTTGGAAATCTCAGTCTGTGAGTTTATTTTGGAGATAAGGTCTCTGCAGATGTA 1798  
Db 1772 ACATCTCTTCTTGGAAATCTCAGTCTGTGAGTTTATTTTGGAGATAAGGTCTCTGCAGATGTA 1831  
Qy 1799 GTTAGTTAAGACAAGTCTCATGCTGGAATGAAGGTAGACCTAAAATTCATATGACTGGTTTC 1858  
Db 1832 GTTAGTTAAGACAAGTCTCATGCTGGAATGAAGGTAGACCTAAAATTCATATGACTGGTTTC 1891  
Qy 1859 CTTGTATGAAAAGGAGAGGACACAGAGACAGAGGAGACGCGGGAAAGACTATATAAGAT 1918  
Db 1892 CTTGTATGAAAAGGAGAGGACACAGAGACAGAGGAGACGCGGGAAAGACTATATAAGAT 1951  
Qy 1919 GAAGGACAGATCGGAGTTTTCGAGCCACAAGCTAAGAAACACCAAGGATTTGTGGCAACC 1978  
Db 1952 GAAGGACAGATCGGAGTTTTCGAGCCACAAGCTAAGAAACACCAAGGATTTGTGGCAACC 2011  
Qy 1979 ATCAGAAGCTTGGAGAGGCAAGAGAAATTTCTTCCCTAGAGGCTTTAGAGGGATAACGG 2038  
Db 2012 ATCAGAAGCTTGGAGAGGCAAGAGAAATTTCTTCCCTAGAGGCTTTAGAGGGATAACGG 2071  
Qy 2039 CTCTGCTGAAACCTTAAATCTCAGACTTCAGAGCTTCAGAGCTCTCTGAAAGAAAGATAAATTTTCG 2098  
Db 2072 CTCTGCTGAAACCTTAAATCTCAGACTTCAGAGCTTCAGAGCTCTCTGAAAGAAAGATAAATTTTCG 2131  
Qy 2099 GCTGTTTAAAGCCACAAGGATAATTTGGTTACAGAGCTCTAGGAACTAATAACAGCTGC 2158  
Db 2132 GCTGTTTAAAGCCACAAGGATAATTTGGTTACAGAGCTCTAGGAACTAATAACAGCTGC 2191  
Qy 2159 TAAATGATCCCTGCTCTCTGCTGTTTACATTTCTGTGTGTGTCCTCCCAAGATGTACC 2218  
Db 2192 TAAATGATCCCTGCTCTCTGCTGTTTACATTTCTGTGTGTGTCCTCCCAAGATGTACC 2251  
Qy 2219 AAAAGTTGCTTTGTGACCCCAATAGAAATATGGCAGAAATGATGCGATGCCACTTCCAAAGAT 2278  
Db 2252 AAAAGTTGCTTTGTGAC - CCAATAGAAATATGGCAGAAATGATGCGATGCCACTTCCAAAGAT 2310  
Qy 2279 TAGGTTATAAAGACATGCGAGCTTCTACTTTCAGCCCTCTCTCTGCGACCCACCGCCC 2338  
Db 2311 TAGGTTATAAAGACATGCGAGCTTCTACTTTCAGCCCTCTCTCTGCGACCCACCGCCC 2370  
Qy 2339 CCAATCTATCTGGCTCACTCGCTCTGGGGAAAGCTAGCTGCGCATGCTATGAGCAGGCT 2398  
Db 2371 CCAATCTATCTGGCTCACTCGCTCTGGGGAAAGCTAGCTGCGCATGCTATGAGCAGGCT 2430  
Qy 2399 ATAAAGAGACTTACCTGGTAAATAAATGAAGTCTCTGCCACAGCAGCACATTTAGTGAACCT 2458  
Db 2431 ATAAAGAGACTTACCTGGTAAATAAATGAAGTCTCTGCCACAGCAGCACATTTAGTGAACCT 2490  
Qy 2459 AGAAGCAGAGACTCTGTGAGATAATCGATGTTGTTGTTT - AAGTTGCTCAGTTTTGCT 2517  
Db 2491 AGAAGCAGAGACTCTGTGAGATAATCGATGTTGTTGTTT - AAGTTGCTCAGTTTTGCT 2550  
Qy 2518 CTAACCTTGTATGACGCAATAGATAAATAATATGACAGAGAAAGAGA 2563  
Db 2551 CTAACCTTGTATGACGCAATAGATAAATAATATGACAGAGAAAGAGA 2596

Patent No. 6426191  
GENERAL INFORMATION:  
APPLICANT: Ford, John  
APPLICANT: Face, Ann  
TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF  
FILE REFERENCE: 28110/36010  
CURRENT APPLICATION NUMBER: US/09/457,626  
CURRENT FILING DATE: 1999-12-08  
EARLIER APPLICATION NUMBER: US 09/417,455  
EARLIER FILING DATE: 1999-10-13  
EARLIER APPLICATION NUMBER: US 09/348,942  
EARLIER FILING DATE: 1999-07-07  
EARLIER APPLICATION NUMBER: PCT/US99/04291  
EARLIER FILING DATE: 1999-04-05  
EARLIER APPLICATION NUMBER: US 09/287,210  
EARLIER FILING DATE: 1999-04-05  
EARLIER APPLICATION NUMBER: US 09/251,370  
EARLIER FILING DATE: 1999-02-17  
EARLIER APPLICATION NUMBER: US 09/229,591  
EARLIER FILING DATE: 1999-01-13  
EARLIER APPLICATION NUMBER: US 09/127,698  
EARLIER FILING DATE: 1998-07-31  
EARLIER APPLICATION NUMBER: US 09/099,818  
EARLIER FILING DATE: 1998-06-19  
EARLIER APPLICATION NUMBER: US 09/082,364  
EARLIER FILING DATE: 1998-05-20  
EARLIER APPLICATION NUMBER: US 09/079,909  
EARLIER FILING DATE: 1998-05-15  
EARLIER APPLICATION NUMBER: US 09/055,010  
EARLIER FILING DATE: 1998-04-03  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 6  
LENGTH: 2648  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-457-626-6

Query Match 97.1%; Score 2488.4; DB 3; Length 2648;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 2550; Conservative 0; Mismatches 11; Indels 5; Gaps 5;  
QY 1 AGGGAGCTACACCCCTGTGGAGCTCAAGATGGTCTCGAGTGGGGCGCTGTGCTCCGAA 60  
DB 33 AGGGAGCTACACCCCTGTGGAGCTCAAGATGGTCTCGAGTGGGGCGCTGTGCTCCGAA 92  
QY 61 TGAAGACTCGGATGAAGAGTGTCTTATCTGCATATTAACAGCTTCTAGCTGGAGGC 120  
DB 93 TGAAGACTCGGATGAAGAGTGTCTTATCTGCATATTAACAGCTTCTAGCTGGAGGC 152  
QY 121 TGCATGCGGGAGGTCATTAAAGGTGAAGATCAGCGTGTCCCAATCGTGGCTGG 180  
DB 153 TGCATGCGGGAGGTCATTAAAGGTGAAGATCAGCGTGTCCCAATCGTGGCTGG 212  
QY 181 ATGCCAGCTGCCCCCGTCATCTGGGTGTCCAGGGTGAAGCCAGTCCCTGTATGTG 240  
DB 213 ATGCCAGCTGCCCCCGTCATCTGGGTGTCCAGGGTGAAGCCAGTCCCTGTATGTG 272  
QY 241 GGGTGGGCGAGGCGCATCTTAACAATAGACAGTGAACATCATGGAGCTCTATCTTG 300  
DB 273 GGGTGGGCGAGGCGCATCTTAACAATAGACAGTGAACATCATGGAGCTCTATCTTG 332  
QY 301 GTGCCAAGATTCAGAGCTTCACTTCTACCGGGGACATGGGGCTCACTCCAGCT 360  
DB 333 GTGCCAAGATTCAGAGCTTCACTTCTACCGGGGACATGGGGCTCACTCCAGCT 392  
QY 361 TCGAGTGGGTGCTTACCGGGGTGCTTCTGTGACCGGTGCTGAAGCCGATCAGCCTG 420  
DB 393 TCGAGTGGGTGCTTACCGGGGTGCTTCTGTGACCGGTGCTGAAGCCGATCAGCCTG 452  
QY 421 TCAGACTACCCAGTCTCCGAGATGTGGTGGTGAATGCCGCCATCAGAGCTTCTACT 480  
DB 453 TCAGACTACCCAGTCTCCGAGATGTGGTGGTGAATGCCGCCATCAGAGCTTCTACT 512

QY 481 TCCAGCAGTGTGACTAGGGCAACCGTCCCGCCCGAGAACTCCCTGGCGAGACCAGCTCGG 540  
DB 513 TCCAGCAGTGTGACTAGGGCAACCGTCCCGCCCGAGAACTCCCTGGCGAGACCAGCTCGG 571  
QY 541 GTGAGGGGTGAGTGAGGAGACCCATGGCGGACAACTCACTCTTCTGCTCTCAGGACCCC 600  
DB 572 GTGAGGGGTGAGTGAGGAGACCCATGGCGGACAACTCACTCTTCTGCTCTCAGGACCCC 631  
QY 601 CAGGTCTGACTTAGTGGGCACTGACCACTTTGCTCTGTTCCAGTCTTGCATAAAAT 660  
DB 632 CAGGTCTGACTTAGTGGGCACTGACCACTTTGCTCTGTTCCAGTCTTGCATAAAAT 691  
QY 661 CTGAGATTGGAGCTCAGTCCAGGGTCTCCCGCACTGGATGGTGTACTGCTGTGGAAC 720  
DB 692 CTGAGATTGGAGCTCAGTCCAGGGTCTCCCGCACTGGATGGTGTACTGCTGTGGAAC 751  
QY 721 CTGTGAAAAACATGTGGGGTAAACTGGGAATAACATGAAAGATTTCTGTGGGGTGG 780  
DB 752 CTGTGAAAAACATGTGGGGTAAACTGGGAATAACATGAAAGATTTCTGTGGGGTGG 811  
QY 781 GTGGGGAGTGTGGGAATCACTTCTGCTTAATGGTAACTGACAACTGTACCCCTGAGCC 840  
DB 812 GTGGGGAGTGTGGGAATCACTTCTGCTTAATGGTAACTGACAACTGTACCCCTGAGCC 871  
QY 841 CGCAGGCGCAACCCATCCCACTTATAGGGTCACTGAGTCTTCCACATGAAGTC 900  
DB 872 CGCAGGCGCAACCCATCCCACTTATAGGGTCACTGAGTCTTCCACATGAAGTC 931  
QY 901 CTCTCACTCAGCTGTGCAGGAGGAGGTGCTATAGAGTCAGGATCATGGCCCT 960  
DB 932 CTGTCACTCAGCTGTGCAGGAGGAGGTGCTATAGAGTCAGGATCATGGCCCT 991  
QY 961 TGGCCCGCCCGCCCTTCCCTTT - ATCTGCCACTGTATATGCTACCTTTCCCTATC 1019  
DB 992 TGGCCCGCCCGCCCTTCCCTTTATCTGCCACTGTATATGCTACCTTTCCCTATC 1051  
QY 1020 TCTTCCCTCATCATCTTCTGTGGGCATGAGGAGTGTGATGTGAGAAATGGTTCG 1079  
DB 1052 TCTTCCCTCATCATCTTCTGTGGGCATGAGGAGTGTGATGTGAGAAATGGTTCG 1111  
QY 1080 AGCTCAGAAGATAAAGATAGTAGGTATGCTGATCTCTTTTAAACCCCAAGATACA 1139  
DB 1112 AGCTCAGAAGATAAAGATAGTAGGTATGCTGATCTCTTTTAAACCCCAAGATACA 1171  
QY 1140 ATCAAAATCCAGATGCTGGTCTCTATTTCCCATGAAAAGTCTCATGACATATTGAGAA 1199  
DB 1172 ATCAAAATCCAGATGCTGGTCTCTATTTCCCATGAAAAGTCTCATGACATATTGAGAA 1231  
QY 1200 GACCTACTTACAAAGTGGCATATA - TTGCAATTTATTTTAAATAAAGATACCTATTTAT 1258  
DB 1232 GACCTACTTACAAAGTGGCATATAATTGCAATTTATTTTAAATAAAGATACCTATTTAT 1291  
QY 1259 ATATTTCTTTATAGAAAAGTCTGGAAGATTTTCTCAATTTGAGCAATCTCAGGGTG 1318  
DB 1292 ATATTTCTTTATAGAAAAGTCTGGAAGATTTTCTCAATTTGAGCAATCTCAGGGTG 1351  
QY 1319 GTGGCAGTATAGTGTGATTTTCTTTTAAATTTCTGTTAAATTTATCTGTTTCTTAAATTTT 1378  
DB 1352 GTGGCAGTATAGTGTGATTTTCTTTTAAATTTCTGTTAAATTTATCTGTTTCTTAAATTTT 1411  
QY 1379 CTACAATGAAGATGAATTTCTTTGATAAATAAAGAAATTAATCTTGAGGTAGC 1438  
DB 1412 CTACAATGAAGATGAATTTCTTTGATAAATAAAGAAATTAATCTTGAGGTAGC 1471  
QY 1439 AGAGCAGACATCATCTCTGATTTGCTCAGCTTCCAAATTTCCCGAGATTAATTTCAAAATG 1498  
DB 1472 AGAGCAGACATCATCTCTGATTTGCTCAGCTTCCAAATTTCCCGAGATTAATTTCAAAATG 1531  
QY 1499 AATCCAGCTCTGCTGCTGTGGTGTGTGTAGTAGTATGATCAGGAAACAGATCTCAGAAAG 1558  
DB 1532 AATCCAGCTCTGCTGCTGTGGTGTGTGTAGTAGTATGATCAGGAAACAGATCTCAGAAAG 1591

QY 1559 CCACTGAGGAGGAGGCTGTGCTGAGTTTGTGTGGCTGGAATCTCTGGGTAAAGAACTTAA 1618  
Db 1592 CCACTGAGGAGGAGGCTGTGCTGAAAGTTGTGTGGCTGGAATCTCTGGGTAAAGAACTTAA 1651  
QY 1619 AGAACAAAATCATCTGGTAAATCTTTCTAGAGGATCACAGCCCTCGGATTCGAAG 1678  
Db 1652 AGAACAAAATCATCTGGTAAATCTTTCTAGAGGATCACAGCCCTCGGATTCGAAG 1711  
QY 1679 CAATGGATCCAGTCTCTAAGAGGCTGTGTAATCTGTTGAATGTGTCCTCCCTCAAAATTC 1738  
Db 1712 CAATGGATCCAGTCTCTAAGAGGCTGTGTAATCTGTTGAATGTGTCCTCCCTCAAAATTC 1771  
QY 1739 ACATCTCTCTTGGATCTCAGTCTGTGAGTTTATTTGGAGATAAGGTCTCTGCAGATGTA 1798  
Db 1772 ACATCTCTCTTGGATCTCAGTCTGTGAGTTTATTTGGAGATAAGGTCTCTGCAGATGTA 1831  
QY 1799 GTTAGTTAAGACAAGTCTAGTGTGAATGAAGTGAACCTAAATCTCAATATGACTGTTTC 1858  
Db 1832 GTTAGTTAAGACAAGTCTAGTGTGAATGAAGTGAACCTAAATCTCAATATGACTGTTTC 1891  
QY 1859 CTTGTATGAAAAGAGAGGACACAGAGACAGAGGAGACCGGGGAAGACTATGTAAAGAT 1918  
Db 1892 CTTGTATGAAAAGAGAGGACACAGAGACAGAGGAGACCGGGGAAGACTATGTAAAGAT 1951  
QY 1919 GAAGCAGAGATCGAGATTTTGCAGCCACAAGCTAAGAAACACCAAGGATTTGTGCAACC 1978  
Db 1952 GAAGCAGAGATCGAGATTTTGCAGCCACAAGCTAAGAAACACCAAGGATTTGTGCAACC 2011  
QY 1979 ATCAGAAGCTTGAAGAGGCAAGAGAAATCTTCCCTAGAGGCTTTAGAGGGATAACGG 2038  
Db 2012 ATCAGAAGCTTGAAGAGGCAAGAGAAATCTTCCCTAGAGGCTTTAGAGGGATAACGG 2071  
QY 2039 CTCTCTCTGAAACCTTAATCTCAGACTTCAGGCTCTCAGGCTCTGAAAGAAAGAAATAAATTCG 2098  
Db 2072 CTCTCTCTGAAACCTTAATCTCAGACTTCAGGCTCTCAGGCTCTGAAAGAAAGAAATAAATTCG 2131  
QY 2099 GCTGTTTTAAGCCACAAGGATAATTTGTTACAGAGCTCTAGGAAAATAATACAGCTGC 2158  
Db 2132 GCTGTTTTAAGCCACAAGGATAATTTGTTACAGAGCTCTAGGAAAATAATACAGCTGC 2191  
QY 2159 TAAATATGATCCCTGTCTCTCTGTTTACATTTCTGTGTGTGTCCTCCCTCCCAATGTACC 2218  
Db 2192 TAAATATGATCCCTGTCTCTCTGTTTACATTTCTGTGTGTGTCCTCCCTCCCAATGTACC 2251  
QY 2219 AAAAGTTGTCTTTGTGACCCCAATAGATAATGAGGAGAGTATGAGGCTTGCACATTCGAAAGT 2278  
Db 2252 AAAAGTTGTCTTTGTGAC - CCAATAGATAATGAGGAGAGTATGAGGCTTGCACATTCGAAAGT 2310  
QY 2279 TAGGTTATAAAGACATCTGAGCTTCTACTTGAAGCTTCTCTCTGAGCCCTCTCTCTGAGCCG 2338  
Db 2311 TAGGTTATAAAGACATCTGAGCTTCTACTTGAAGCTTCTCTCTGAGCCCTCTCTCTGAGCCG 2370  
QY 2339 CCAATCTATCTTGTGCTCACTCGCTCTGGGGAGAGTATGAGTGCATGCTATGAGGAGGCT 2398  
Db 2371 CCAATCTATCTTGTGCTCACTCGCTCTGGGGAGAGTATGAGTGCATGCTATGAGGAGGCT 2430  
QY 2399 ATAAAGAGACTTACGTGGTAAAAATGAAAGTCTCTGCCCCCAGGACCAATTAAGTGAACCT 2458  
Db 2431 ATAAAGAGACTTACGTGGTAAAAATGAAAGTCTCTGCCCCCAGGACCAATTAAGTGAACCT 2490  
QY 2459 AGAAGCAGAGACTCTGTGAGATAATCGATGTTGTTGTTTT - AAGTTGCTCAGTTTTGCT 2517  
Db 2491 AGAAGCAGAGACTCTGTGAGATAATCGATGTTGTTGTTTTAAGTTGCTCAGTTTTGCT 2550  
QY 2518 CTAACCTGTTATGAGCAATAGATAATAATATATGAGCAAGAAAGAGA 2563  
Db 2551 CTAACCTGTTATGAGCAATAGATAATAATATATGAGCAAGAAAGAGA 2596

RESULT 5

US-09-576-008-6

; Sequence 6, Application US/09576008

; Patent No. 6541623

GENERAL INFORMATION:

; APPLICANT: Ford, John

; APPLICANT: Ho, Alice Suk-Yue

; APPLICANT: Pace, Ann

; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF

; FILE REFERENCE: 28110/36456

; CURRENT APPLICATION NUMBER: US/09/576,008

; CURRENT FILING DATE: 2000-05-22

; PRIOR APPLICATION NUMBER: US 09/523,552

; PRIOR FILING DATE: 2000-03-10

; PRIOR APPLICATION NUMBER: US 09/457,626

; PRIOR FILING DATE: 1999-12-08

; PRIOR APPLICATION NUMBER: US 09/417,455

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: US 09/348,942

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: PCT/US99/04291

; PRIOR FILING DATE: 1999-04-05

; PRIOR APPLICATION NUMBER: US 09/287,210

; PRIOR FILING DATE: 1999-04-05

; PRIOR APPLICATION NUMBER: US 09/251,370

; PRIOR FILING DATE: 1999-02-17

; PRIOR APPLICATION NUMBER: US 09/229,591

; PRIOR FILING DATE: 1999-01-13

; PRIOR APPLICATION NUMBER: US 09/127,698

; PRIOR FILING DATE: 1998-07-31

; PRIOR APPLICATION NUMBER: US 09/099,818

; PRIOR FILING DATE: 1998-06-19

; PRIOR APPLICATION NUMBER: US 09/082,364

; PRIOR FILING DATE: 1998-05-20

; PRIOR APPLICATION NUMBER: US 09/079,909

; PRIOR FILING DATE: 1998-05-15

; PRIOR APPLICATION NUMBER: US 09/055,010

; PRIOR FILING DATE: 1998-04-03

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 6

; LENGTH: 2648

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-576-008-6

Query Match 97.1%; Score 2488.4; DB 4; Length 2648;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 2550; Conservative 0; Mismatches 11; Indels 5; Gaps 5;

QY 1 AGGGAGGCTCACACCTGTGGAGCTCAAGATGGTCTGAGTGGGGCGCTGTCTCCGAA 60

Db 33 AGGGAGGCTCACACCTGTGGAGCTCAAGATGGTCTGAGTGGGGCGCTGTCTCCGAA 92

QY 61 TGAAGGACTCGGCATTGAAGGTGCTTTTATCTGCATAATAACCAAGCTTTCTAGCTGGAGGC 120

Db 93 TGAAGGACTCGGCATTGAAGGTGCTTTTATCTGCATAATAACCAAGCTTTCTAGCTGGAGGC 152

QY 121 TGCATGCGAGGAAGGTCAATTAAGGTGAAGAGATCAAGTGTGTCCTCCCAATCGGTGCTGG 180

Db 153 TGCATGCGAGGAAGGTCAATTAAGGTGAAGAGATCAAGTGTGTCCTCCCAATCGGTGCTGG 212

QY 181 ATGCCAGCTGTCCCCCGTCATCTGGGTGTCAGGCTGGAAGCCAGCTGCTCATGTG 240

Db 213 ATGCCAGCTGTCCCCCGTCATCTGGGTGTCAGGCTGGAAGCCAGCTGCTCATGTG 272

QY 241 GGGTGGGGCAGGAGCGGACTCTAAACATAGAGCCAGTGAACATCATGGAGCTCTATCTTG 300

Db 273 GGGTGGGGCAGGAGCGGACTCTAAACATAGAGCCAGTGAACATCATGGAGCTCTATCTTG 332

QY 301 GTGCCAAGGAATCCAAAGAGCTTCACTTCTACCGCGGGAATGGGGCTCACTCCAGCT 360

Db 333 GTGCCAAGGAATCCAAAGAGCTTCACTTCTACCGCGGGAATGGGGCTCACTCCAGCT 392

QY 361 TCGAGTGGCTGCTTACCCGGGCTGGTCTGTGACCGGTGCTGAGCCGATCAGCCTG 420

Db 393 TCGAGTGGCTGCTTACCCGGGCTGGTCTGTGACCGGTGCTGAGCCGATCAGCCTG 452





RESULT 6  
US-09-949-016-956  
; Sequence 956, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 956  
; LENGTH: 2720  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-956

Query Match  
Best Local Similarity 97.1%; Score 2488.4; DB 4; Length 2720;  
Matches 2550; Conservative 0; Mismatches 11; Indels 5; Gaps 5;

QY	1	AGGGAGCTACACCTCTGGAGCTCAAGATGGTCTCAGTGGGGCGTGTCTCCGAA	60
DB	134	AGGGAGCTACACCTCTGGAGCTCAAGATGGTCTCAGTGGGGCGTGTCTCCGAA	193
QY	61	TGAAGGATCGGCATGAAGTGTCTTATCTGCATAAACCAGCTTCTAGCTGGAGGC	120
DB	194	TGAAGGATCGGCATGAAGTGTCTTATCTGCATAAACCAGCTTCTAGCTGGAGGC	253
QY	121	TGCATGCGAGGAAGTCAATTAAGTGAAGAGATCAGCGTGTGCCAATCGTGGCTGG	180
DB	254	TGCATGCGAGGAAGTCAATTAAGTGAAGAGATCAGCGTGTGCCAATCGTGGCTGG	313
QY	181	ATGCCAGCTGTCCCGCTCATCTGGGTGTCCAGGTGGAGCCAGTGCCTGTATGTG	240
DB	314	ATGCCAGCTGTCCCGCTCATCTGGGTGTCCAGGTGGAGCCAGTGCCTGTATGTG	373
QY	241	GGGTGGGCGAGGCGGACTCTAACACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG	300
DB	374	GGGTGGGCGAGGCGGACTCTAACACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG	433
QY	301	GTGCCAAGGAATCCAGAGCTTCACTTTCTACCGCGGGACATGGGGCTCACCTCCAGCT	360
DB	434	GTGCCAAGGAATCCAGAGCTTCACTTTCTACCGCGGGACATGGGGCTCACCTCCAGCT	493
QY	361	TGAGTGGGCTGCTTACCGGGCTGGTTCCTGTGACCGGTGCTGAAGCCGATCAGCCTG	420
DB	494	TGAGTGGGCTGCTTACCGGGCTGGTTCCTGTGACCGGTGCTGAAGCCGATCAGCCTG	553
QY	421	TCAGACTACCCAGCTTCCCGGAATGGTGGCTGGAATGCCCGCCATCAGACTTCTACT	480
DB	554	TCAGACTACCCAGCTTCCCGGAATGGTGGCTGGAATGCCCGCCATCAGACTTCTACT	613
QY	481	TCCAGCAGTGTGACTAGGGCAACGTGCCCGCCAGAACTCCCTGGGCGAGCCAGCTCGG	540
DB	614	TCCAGCAGTGTGACTAGGGCAACGTGCCCGCCAGAACTCCCTGGGCGAGCCAGCTCGG	672
QY	541	GTAGGGGTGTGTGAGAGACCCATGGCGGCAATCACTCTTTCTGTCTCAGACCCC	600
DB	673	GTAGGGGTGTGTGAGAGACCCATGGCGGCAATCACTCTCTGTCTCAGACCCC	732
QY	601	CAGGTCGACTAGTGGGCGGCTGACCTTGTCTTCTGGTTCCAGTTTGCATAAATT	660
DB	733	CAGGTCGACTAGTGGGCGGCTGACCTTGTCTTCTGGTTCCAGTTTGCATAAATT	792

QY	661	CTGAGATTTGGAGCTCAGTCCAGGGTCTCTCCCGCACTGGATGGTCTACTGCTGTGAAC	720
DB	793	CTGAGATTTGGAGCTCAGTCCAGGGTCTCTCCCGCACTGGATGGTCTACTGCTGTGAAC	852
QY	721	CTTTGAAAAACCATGTGGGTAAATCGGGAATAAATGAAAAATTTCTGTGGGGTGGG	780
DB	853	CTTTGAAAAACCATGTGGGTAAATCGGGAATAAATGAAAAATTTCTGTGGGGTGGG	912
QY	781	GTGGGGAGTGTGGGAATCAATCTCTGCTTAATGTGTAACAAAGTGTACCTGAGCC	840
DB	913	GTGGGGAGTGTGGGAATCAATCTCTGCTTAATGTGTAACAAAGTGTACCTGAGCC	972
QY	841	CGCAGGCGCAACCCATCCCGAGTTCAGGCTTATAGGCTCAGTCTCTCCATGAAGTC	900
DB	973	CGCAGGCGCAACCCATCCCGAGTTCAGGCTTATAGGCTCAGTCTCTCCATGAAGTC	1032
QY	901	CTCTCACTCACCACCTGTGCAGGAGAGGAGGTGGTCAATAGAGTCAGGGATCTATGCCCT	960
DB	1033	CTGTCACTCACCACCTGTGCAGGAGAGGAGGTGGTCAATAGAGTCAGGGATCTATGCCCT	1092
QY	961	TGGCCAGCCCGCCCTTCCCTTT-ATCTGCGCACTGTCTCATATGCTACCTTTCTCTATC	1019
DB	1093	TGGCCAGCCCGCCCTTCCCTTTAATCTGCGCACTGTCTCATATGCTACCTTTCTCTATC	1152
QY	1020	TCTTCCCTCATCATCTTGTGTGGCATGAGAGGTGGTGTGATGTGAGAAGAAATGTTGCG	1079
DB	1153	TCTTCCCTCATCATCTTGTGTGGCATGAGAGGTGGTGTGATGTGAGAAGAAATGTTGCG	1212
QY	1080	AGCTCAGAAGATAAAGATAGTAGGTATGCTGATCTCTTTTAAAAACCCAAAGATACA	1139
DB	1213	AGCTCAGAAGATAAAGATAGTAGGTATGCTGATCTCTTTTAAAAACCCAAAGATACA	1272
QY	1140	ATCAAAATCCAGATGTGGTCTCTATTCCCATGAAAGAGTCTCATGACATATTGAGAA	1199
DB	1273	ATCAAAATCCAGATGTGGTCTCTATTCCCATGAAAGAGTCTCATGACATATTGAGAA	1332
QY	1200	GACCTACTTACAAAGTGGCATATA-TTGCATTTTATTTTAAATAAAGATACCTATTAT	1258
DB	1333	GACCTACTTACAAAGTGGCATATA-TTGCATTTTATTTTAAATAAAGATACCTATTAT	1392
QY	1259	ATATTTCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTTGTAGCAATGTGAGGTG	1318
DB	1393	ATATTTCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTTGTAGCAATGTGAGGTG	1452
QY	1319	GTGGCAGTATAGTGAATTTTCTTTTAAATTTCTGTTAAATTTATCTGTTTCTTAATTTT	1378
DB	1453	GTGGCAGTATAGTGAATTTTCTTTTAAATTTCTGTTAAATTTATCTGTTTCTTAATTTT	1512
QY	1379	CTCAATGAAGATGAATTCCTTGTATATAAATAAAGAAAGAAATTAATCTTGAGGTAAAG	1438
DB	1513	CTCAATGAAGATGAATTCCTTGTATATAAATAAAGAAAGAAATTAATCTTGAGGTAAAG	1572
QY	1439	AGAGCAGACATCATCTCTGATGTCTCAGCCTCAATTTCCCGAGAGTAAATTTCAATTTG	1498
DB	1573	AGAGCAGACATCATCTCTGATGTCTCAGCCTCAATTTCCCGAGAGTAAATTTCAATTTG	1632
QY	1499	AATCGAGCTCTGCTCTCTGTTGTTGTAGTAGTGTGATCAGGAAACAGATCTCAGCAAG	1558
DB	1633	AATCGAGCTCTGCTCTCTGTTGTTGTAGTAGTGTGATCAGGAAACAGATCTCAGCAAG	1692
QY	1559	CACTGAGGAGAGCTGTGCTGATGTTGTGTGGTGGAAATCTCTGGGTAAAGAACTTAA	1618
DB	1693	CACTGAGGAGAGCTGTGCTGATGTTGTGTGGTGGAAATCTCTGGGTAAAGAACTTAA	1752
QY	1619	AGACAAAAATCATCTGTTAAATTTCTTCTAGAGGATCAGACCCCTGGGATTTCAAGG	1678
DB	1753	AGACAAAAATCATCTGTTAAATTTCTTCTAGAGGATCAGACCCCTGGGATTTCAAGG	1812
QY	1679	CATTGGATCCAGTCTCTAAGAGGCTGTGTTACTGTTGAAATTTGTCTCCCTCAAAATTC	1738
DB	1813	CATTGGATCCAGTCTCTAAGAGGCTGTGTTACTGTTGAAATTTGTCTCCCTCAAAATTC	1872
QY	1739	ACATCCTTTTGGAAATCTCAGTCTGTGATTTATTTGGAGATGAAGGTCTCTGCAGATGA	1798









CURRENT FILING DATE: 1999-10-13		86.6%; Score 2220.4; DB 3; Length 7605;	
PRIOR FILING DATE: 1999-07-07		Best Local Similarity 99.1%; Pred. No. 0;	
PRIOR APPLICATION NUMBER: PCT/US99/04291		Matches 2274; Conservative 0; Mismatches 16; Indels 4; Gaps 4;	
PRIOR FILING DATE: 1999-04-05			
PRIOR APPLICATION NUMBER: US 09/287,210			
PRIOR FILING DATE: 1999-04-05			
PRIOR APPLICATION NUMBER: US 09/251,370			
PRIOR FILING DATE: 1999-02-17			
PRIOR APPLICATION NUMBER: US 09/229,591			
PRIOR FILING DATE: 1999-01-13			
PRIOR APPLICATION NUMBER: US 09/127,698			
PRIOR FILING DATE: 1998-07-31			
PRIOR APPLICATION NUMBER: US 09/099,818			
PRIOR FILING DATE: 1998-06-19			
PRIOR APPLICATION NUMBER: US 09/082,364			
PRIOR FILING DATE: 1998-05-20			
PRIOR APPLICATION NUMBER: US 09/079,909			
PRIOR FILING DATE: 1998-05-15			
PRIOR APPLICATION NUMBER: US 09/055,010			
PRIOR FILING DATE: 1998-04-03			
NUMBER OF SEQ ID NOS: 30			
SOFTWARE: Fast-Seq for Windows Version 3.0			
SEQ ID NO 8			
LENGTH: 7605			
TYPE: DNA			
ORGANISM: Homo sapiens			
US-09-417-455-8			
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QY	331	ACCGGGGAGACATGCGGCTCACTCAGCTTCAAGTCCGCTGCTCAACCGGGTGGTTCC	390
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QY	391	TGTGACGGTCCCTGAAGCCGATCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCT	450
DB	5225	TGTGACGGTCCCTGAAGCCGATCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCT	5284
QY	451	GCTGGAATGCCCCATCACAGACTTCTACTTCCAGCAGTGTGACTAGGGCAAGCTGCC	510
DB	5285	GCTGGAATGCCCCATCACAGACTTCTACTTCCAGCAGTGTGACTAGGGCAAGCTGCC	5343
QY	511	CCAGAACTCCCTGGGAGAGCCAGCTCGGGTGAAGGGTGAAGTGGAGAGACCCATGGCG	570
DB	5344	CCAGAACTCCCTGGGAGAGCCAGCTCGGGTGAAGGGTGAAGTGGAGAGACCCATGGCG	5403
QY	571	GACAACTACTCTTTCTGCTCTCAGGACCCCGAGCTCTGACTTAGTGGGCACTGACACT	630
DB	5404	GACAACTACTCTCTGCTCTCAGGACCCCGAGCTCTGACTTAGTGGGCACTGACACT	5463
QY	631	TTGCTCTCGGTTCCAGTTTGATATAATCTCAGATTTTGAGCTCAGTCCAGGGTCCCTC	690
DB	5464	TTGCTCTCGGTTCCAGTTTGATATAATCTCAGATTTTGAGCTCAGTCCAGGGTCCCTC	5523
QY	691	CCCACTGGATGGTGTACTGCTGTGGAACCTTTGTAAACCAATCTGGGGTAAACTGGGA	750
DB	5524	CCCACTGGATGGTGTACTGCTGTGGAACCTTTGTAAACCAATCTGGGGTAAACTGGGA	5583
QY	751	ATAACATGAAGAATTTCTGTGGGGTGGGGTGGGGAGTGTGGGAATCATTTCTGCTT	810
DB	5584	ATAACATGAAGAATTTCTGTGGGGTGGGGTGGGGAGTGTGGGAATCATTTCTGCTT	5643
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DB	5644	AATGGTAACGACAGTGTACCTGAGCCCGCCAGCCCAACCCATCCCGAGTTGAGCCT	5703
QY	871	TATAGGTCAGTAGCTCTCCACATGAAGTCTCTCACTCAACCTCTGCGAGAGAGGAG	930
DB	5704	TATAGGTCAGTAGCTCTCCACATGAAGTCTCTCACTCAACCTCTGCGAGAGAGGAG	5763
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DB	5764	GTGGTCATAGAGTCAGGATCTATGGCCCTTGGCCAGCCCCCAACCCCTTCCCTTT	5823
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QY	1170	CATGAAAAAGTCTCATGACATATTGAGAAAGACCTTCTTCAAAAGTGGCATATATTGCAA	1229
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DB	6124	TTTACTTCAATTTAGCAATGTGAGGTTGGTGGCAGTATAGGTGATTTTCTTTAATTC	6183
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QY	1650	GAGGATCAGAGCCCTGGGATTTCCAGGCAATGGATCCAGTCTCTAAAGAGGCTGCTGT	1709
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DB	6603	TATTTGGAGATGAAGTCTCTGCGATGTAGTTTAAAGCAAGGTCATGCTGGATGAAG	6662
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DB	6723	AGGAGACGGGGGAGAACTATGTAAAGATGAAGGACAGATCGGAGTTTTCAGCCACAA	6782
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RESULT 10
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; Sequence 8, Application US/09348942
; Patent No. 6337072
; GENERAL INFORMATION:
; APPLICANT: John Ford
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/35801
; CURRENT APPLICATION NUMBER: US/09/348,942
; CURRENT FILING DATE: 1999-07-07
; EARLIER APPLICATION NUMBER: PCT/US99/04291
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/287,210
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/251,370
; EARLIER FILING DATE: 1999-02-17
; EARLIER APPLICATION NUMBER: US 09/229,591
; EARLIER FILING DATE: 1999-01-13
; EARLIER APPLICATION NUMBER: US 09/127,698
; EARLIER FILING DATE: 1998-07-31
; EARLIER APPLICATION NUMBER: US 09/099,818
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: US 09/082,364
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: US 09/079,909
; EARLIER FILING DATE: 1998-05-15
; EARLIER APPLICATION NUMBER: US 09/055,010
; EARLIER FILING DATE: 1998-04-03
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; LENGTH: 7605
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; ORGANISM: Homo sapiens
US-09-348-942-8

Query Match      86.6%; Score 2220.4; DB 3; Length 7605;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 2274; Conservative 0; Mismatches 16; Indels 4; Gaps 4;

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Qy 1710 ACTGGTTGAATTTGTCTCCCTTCAAAATTCACATCTTTTGGAACTCTCAGTCTGTGAGTT 1769  
Db 6543 ACTGGTTGAATTTGTCTCCCTTCAAAATTCACATCTTTTGGAACTCTCAGTCTGTGAGTT 6602  
Qy 1770 TATTTGGAGATAAGGCTCTCTGCAGATGTAGTTAGTTAAGACAAGTCTATGCTGGAATGAAG 1829  
Db 6603 TATTTGGAGATAAGGCTCTCTGCAGATGTAGTTAGTTAAGACAAGTCTATGCTGGAATGAAG 6662  
Qy 1830 GTAGACCTAAATTCATATGATGCTGTTCTCTGTATGAAAAGGAGAGCAGCAGAGACAG 1889  
Db 6663 GTAGACCTAAATTCATATGATGCTGTTCTCTGTATGAAAAGGAGAGCAGCAGAGACAG 6722  
Qy 1890 AGGAGACGCGGGAAAGACTATGTAAAGATGAAGGAGAGATCGGAGTTTTCAGAGCCACAA 1949  
Db 6723 AGGAGACGCGGGAAAGACTATGTAAAGATGAAGGAGAGATCGGAGTTTTCAGAGCCACAA 6782  
Qy 1950 GCTAAGAAACACCAAGGATTTGGCAACCATCAGAGCTTGGAGAGGCAAGAAAGATTT 2009  
Db 6783 GCTAAGAAACACCAAGGATTTGGCAACCATCAGAGCTTGGAGAGGCAAGAAAGATTT 6842  
Qy 2010 CTTTCCCTAGAGCTTTAGAGGGATAACGGCTCTGCTGAAACCTTAATCTCAGACTTCCAG 2069  
Db 6843 CTTTCCCTAGAGCTTTAGAGGGATAACGGCTCTGCTGACACTTAATCTCAGACTTCCAG 6902  
Qy 2070 CTTCTGAAACGAGAAAGAAATAATTTTCGGCTGTTTAAAGCCCAAGGATAATTTGGTTA 2129  
Db 6903 CTTCTGAAACGAGAAAGAAATAATTTTCGGCTGTTTAAAGCCCAAGGATAATTTGGTTA 6962  
Qy 2130 CAGCAGCTCTAGGAAACTTAATACAGCTGCTTAAATGATCCCTGCTCTCTCTGTTTACAT 2189  
Db 6963 TGGCAGCTCTAGGAAACTTAATACAGCTGCTTAAATGATCCCTGCTCTCTCTGTTTACAT 7022  
Qy 2190 TCTGTGTGTCTCCCTCCCAATGTACCAAAGTTGTCTTTGTGACCCCAATAGAAATATGG 2249  
Db 7023 TCTGTGTGTCTCCCTCCCAATGTACCAAAGTTGTCTTTGTGAC -CCATAGAAATATGG 7081  
Qy 2250 CAGAAGTATGGCATGGCACTTCCAGATTAAGTTAATAAAGACACTGCACTTCTACTT 2309  
Db 7082 CAGAAGTATGGCATGGCACTTCCAGATTAAGTTAATAAAGACACTGCACTTCTACTT 7141  
Qy 2310 GAGCCCTCTCTCTGCGCACCCACCGCCCAATCTATCTTGGCTCACTCGCTCTGGGGG 2369  
Db 7142 GAGCCCTCTCTCTGCGCACCCACCGCCCAATCTATCTTGGCTCACTCGCTCTGGGGG 7201  
Qy 2370 AAGCTAGCTGCTGCTATGAGCAGGCTTATAAAGAGACTTACGTTGGTAAAAAATGAAGT 2429  
Db 7202 AAGCTAGCTTCCATGCTATGAGCAGGCTTATAAAGAGACTTATGTTGGTAAAAAATGAAGT 7261  
Qy 2430 CTCTGCGCCACAGCCCAATTAGTGAACTTAGAGCAGAGACTCTGTGAGATAATTCGATGT 2489  
Db 7262 CTCTGCGCCACAGCCCAATTAGTGAACTTAGAGCAGAGACTCTGTGAGATAATTCGATGT 7321  
Qy 2490 TTGTTGTTTTAAGTTGCTCAGTTTGGTCTAACTTTGTTATGACGCAATAGATAAATAA 2549  
Db 7322 TTGTTGTTTTAAGTTGCTCAGTTTGGTCTAACTTTGTTATGACGCAATAGATAAATAA 7381



QY	2550	TGCAGAGAAAGAGA	2563	Db	5344	CCAGAACTCCCTGGGCAGAGCCAGCTCGGGTGAGGGGTGAGTGAGGAGAACCCATGGCG	5403
Db	7382	TGCAGAGAAAGAGA	7395	QY	571	GACAACTACTCTTTCTGCTCTCAGGACCCCGAGGCTCTGACTTAGTGGGACACTGACCACT	630
				Db	5404	GACAACTACTCTCTGCTCTCAGGACCCCGAGGCTCTGACTTAGTGGGACACTGACCACT	5463
				QY	631	TTGTCTTCTGGTTCCAGTTTGCATAAATCTGAGATTTGGAGCTCAGTCCAGGGCTCTC	690
				Db	5464	TTGTCTTCTGGTTCCAGTTTGCATAAATCTGAGATTTGGAGCTCAGTCCAGGGCTCTC	5523
				QY	691	CCCCACTGGATGGTCTACTGCTGTGGAAACCTTTGTAAAAACCATGTGGGGTAAACTGGGA	750
				Db	5524	CCCCACTGGATGGTCTACTGCTGTGGAAACCTTTGTAAAAACCATGTGGGGTAAACTGGGA	5583
				QY	751	ATAACATGAAAAAGATTTCTGTGGGGTGGGGTGGGGGAGTGTGGGAAATCATTCCTGCTT	810
				Db	5584	ATAACATGAAAAAGATTTCTGTGGGGTGGGGTGGGGGAGTGTGGGAAATCATTCCTGCTT	5643
				QY	811	AATGGTAACTGACAGTGTACCCCTGAGCCCGCAGGCCCAACCATCCCCAGTTGAGCCT	870
				Db	5644	AATGGTAACTGACAGTGTACCCCTGAGCCCGCAGGCCCAACCATCCCCAGTTGAGCCT	5703
				QY	871	TATAGGCTCAGTAGCTCTCCACATGAAGTCTCTCACTCACCACCTGTGCAGGAGAGGAG	930
				Db	5704	TATAGGCTCAGTAGCTCTCCACATGAAGTCTCTCACTCACCACCTGTGCAGGAGAGGAG	5763
				QY	931	GTGGTCATAGAGTCAGGATCTATGGCCCTTGGCCCGCAGCCCAACCCCTTCCCTT-ATC	989
				Db	5764	GTGGTCATAGAGTCAGGATCTATGGCCCTTGGCCCGCAGCCCAACCCCTTCCCTTAAATC	5823
				QY	990	CTGCCACTGTCTATGCTTACCTTCTCTATCTCTTCCCTCATCATCTTGTGGGATGA	1049
				Db	5824	CTGCCACTGTCTATGCTTACCTTCTCTATCTCTTCCCTCATCATCTTGTGGGATGA	5883
				QY	1050	GGAGGTGGTGTGTGTCAGAAAGAAATGGTTCGAGCTCAGAAAGATAAAGATAAGTAGGTAT	1109
				Db	5884	GGAGGTGGTGTGTGTCAGAAAGAAATGGTTCGAGCTCAGAAAGATAAAGATAAGTAGGTAT	5943
				QY	1110	GCTGATCTCTTTTAAAAACCCCAAGATACAATCAAAATCCAGATGCTGGTCTCTATTC	1169
				Db	5944	GCTGATCTCTTTTAAAAACCCCAAGATACAATCAAAATCCAGATGCTGGTCTCTATTC	6003
				QY	1170	CATGAAAAAGTGTCTATGACATATTCAGAAAGACCTTCTTACAAAGTGGATATATTGCAA	1229
				Db	6004	CATGAAAAAGTGTCTATGACATATTCAGAAAGACCTTCTTACAAAGTGGATATATTGCAA	6063
				QY	1230	TTTATTTTAAATAAGATACCTATTATATATTTCTTTATAGAAAAAGTCTGGAGAG	1289
				Db	6064	TTTATTTTAAATAAGATACCTATTATATATTTCTTTATAGAAAAAGTCTGGAGAG	6123
				QY	1290	TTTACTTCAATTTGTAGCAATGTCCAGGTGGTGGCAGTATAGGTGATTTTCTTTTAAATTC	1349
				Db	6124	TTTACTTCAATTTGTAGCAATGTCCAGGTGGTGGCAGTATAGGTGATTTTCTTTTAAATTC	6183
				QY	1350	TGTTAATTTATCTGATTTTCTTAATTTTCTACAATGAAGATGAATCTCTGTATATAAAA	1409
				Db	6184	TGTTAATTTATCTGATTTTCTTAATTTTCTACAATGAAGATGAATCTCTGTATATAAAA	6243
				QY	1410	TAAGAAAAAGAAATTAATCTTTGAGGTAAGCAGAGCAGACATCTCTGATTTGCTCAGC	1469
				Db	6244	TAAGAAAAAGAAATTAATCTTTGAGGTAAGCAGAGCAGACATCTCTGATTTGCTCAGC	6302
				QY	1470	CTCCAAATCCCGAGAGTAAATTCAAATTCGAATTCGAGCTCTGCTGCTCTGGTGGTGTAG	1529
				Db	6303	CTCCAAATCCCGAGAGTAAATTCAAATTCGAATTCGAGCTCTGCTGCTCTGGTGGTGTAG	6362
				QY	1530	TAGTGATCAGGAAACAGATCTCAGCAAGCCACTGAGGAGGAGGCTGTGCTGATTTGTG	1589
				Db	6363	TAGTGATCAGGAAACAGATCTCAGCAAGCCACTGAGGAGGAGGCTGTGATGATTTGTG	6422
				QY	1590	TGGCTGGAATCTCTGGGTAAGGAATCTTAAAGAAACAAAAATCATCTCGTAAATTTCTTCTA	1649
				Db	6423	TGGCTGGAATCTCTGGGTAAGGAATCTTAAAGAAACAAAAATCATCTCGTAAATTTCTTCTA	6482

RESULT 12  
US-09-576-008-8  
; Sequence 8, Application US/09576008  
; Patent No. 6541623  
; GENERAL INFORMATION:  
; APPLICANT: Ford, John  
; APPLICANT: Ho, Alice Suk-Yue  
; APPLICANT: Pace, Ann  
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF  
; FILE REFERENCE: 28110/36456  
; CURRENT APPLICATION NUMBER: US/09/576,008  
; CURRENT FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: US 09/523,552  
; PRIOR FILING DATE: 2000-03-10  
; PRIOR APPLICATION NUMBER: US 09/457,626  
; PRIOR FILING DATE: 1999-12-08  
; PRIOR APPLICATION NUMBER: US 09/417,455  
; PRIOR FILING DATE: 1999-10-13  
; PRIOR APPLICATION NUMBER: US 09/348,942  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: PCT/US99/04291  
; PRIOR FILING DATE: 1999-04-05  
; PRIOR APPLICATION NUMBER: US 09/287,210  
; PRIOR FILING DATE: 1999-04-05  
; PRIOR APPLICATION NUMBER: US 09/251,370  
; PRIOR FILING DATE: 1999-02-17  
; PRIOR APPLICATION NUMBER: US 09/229,591  
; PRIOR FILING DATE: 1999-01-13  
; PRIOR APPLICATION NUMBER: US 09/127,698  
; PRIOR FILING DATE: 1998-07-31  
; PRIOR APPLICATION NUMBER: US 09/099,818  
; PRIOR FILING DATE: 1998-06-19  
; PRIOR APPLICATION NUMBER: US 09/082,364  
; PRIOR FILING DATE: 1998-05-20  
; PRIOR APPLICATION NUMBER: US 09/079,909  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: US 09/055,010  
; PRIOR FILING DATE: 1998-04-03  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 7605  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-576-008-8

Query Match	86.6%	Score	2220.4	DB 4	Length	7605
Best Local Similarity	95.1%	Pred. No. 0				
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					Gaps	4
QY	271	AGCCAGTGAACATCATGGAGCTCTATCTGGTCCCAAGGAATCCAAAGAGCTTCACCTTCT	330			
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QY	331	ACCGGGGACATGGGGCTCACTCAGCTTCAGGTCGGCTGCTACCCGGGCTGGTTC	390			
Db	5165	ACCGGGGACATGGGGCTCACTCAGCTTCAGGTCGGCTGCTACCCGGGCTGGTTC	5224			
QY	391	TGTGACGGTGGCTGAAGCGGATCAGCTGTGAGCTCACCAGCTTCCGAGAAATGGTG	450			
Db	5225	TGTGACGGTGGCTGAAGCGGATCAGCTGTGAGCTCACCAGCTTCCGAGAAATGGTG	5284			
QY	451	GCTGGAAATGCCCATCACAGCTTCTACTTCCAGCAGTGTGACTAGGCGCAAGCTGCC	510			
Db	5285	GCTGGAAATGCCCATCACAGCTTCTACTTCCAGCAGTGTGACTAGGCGCAAGCTGCC	5343			
QY	511	CCAGAACTCCTCTGGGAGAGCCAGCTCGGGTGAGGGGTGAGTGGAGGAGACCCATGGCG	570			

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QY 1650 GAAGGATCACAGCCCTGGGATTCGAAGGCAATGGATCCAGTCTCTAAGAAGGCTGCTGT 1709
DB 6483 GAAGGATCACAGCCCTGGGATTCGAAGGCAATGGATCCAGTCTCTAAGAAGGCTGCTGT 6542
QY 1710 ACTGGTTGAATGTGTGTCCTCCCTCAAAATTCACATCCTCTTGGAACTCAGTCTGTGAGTT 1769
DB 6543 ACTGGTTGAATGTGTGTCCTCCCTCAAAATTCACATCCTCTTGGAACTCAGTCTGTGAGTT 6602
QY 1770 TATTTGGAGATAAGGTCTCTGAGATGTAGTTAGTTAAGCAAGGTCATGCTGGATGAAG 1829
DB 6603 TATTTGGAGATAAGGTCTCTGAGATGTAGTTAGTTAAGCAAGGTCATGCTGGATGAAG 6662
QY 1830 GTAGACCTAAATTCATATGACTGGTTTCCTTGTATGAAGGAGGAGACACAGACAG 1889
DB 6663 GTAGACCTAAATTCATATGACTGGTTTCCTTGTATGAAGGAGGAGACACAGACAG 6722
QY 1890 AGGAGACGGGGGAAGACTATGTAAGATGAAGGACAGATCGGAGTTTTCGAGCCACAA 1949
DB 6723 AGGAGACGGGGGAAGACTATGTAAGATGAAGGACAGATCGGAGTTTTCGAGCCACAA 6782
QY 1950 GCTAAGCAACACCAAGGATTTGGCAACCATCAGAAGCTTTGGAAGAGGCAAAAGAAAT 2009
DB 6783 GCTAAGCAACACCAAGGATTTGGCAACCATCAGAAGCTTTGGAAGAGGCAAAAGAAAT 6842
QY 2010 CTTCCCTAGAGGCTTTAGAGGGATAACGGCTCTGCTGAAACCTTAATCTCAGACTTTCCAG 2069
DB 6843 CTTCCCTAGAGGCTTTAGAGGGATAACGGCTCTGCTGACACCTTAATCTCAGACTTTCCAG 6902
QY 2070 CTTCTGAAAGAAAGAAATAAATTTTCGGCTGTTTTTAAGCCACCAAGGATTAATGGTTA 2129
DB 6903 CTTCTGAAAGAAAGAAATAAATTTTCGGCTGTTTTTAAGCCACCAAGGATTAATGGTTA 6962
QY 2130 CAGCAGCTCTAGAACTAATCAGCTGCTGAAATGATCCCTGCTCCTCGTGTTCATAT 2189
DB 6963 TGGCAGCTCTAGAACTAATCAGCTGCTGAAATGATCCCTGCTCCTCGTGTTCATAT 7022
QY 2190 TCTGTGTGTCTCCCTCCCAATGTACCAAGTTGCTGTTTGTGACCCCAATAGAATATGG 2249
DB 7023 TCTGTGTGTCTCCCTCCCAATGTACCAAGTTGCTGTTTGTGACCCCAATAGAATATGG 7081
QY 2250 CAGAAGTATGGATGCGCATCTTCCAAAGATTAGTTATAAAGACACTGAGCTTCTACTT 2309
DB 7082 CAGAAGTATGGATGCGCATCTTCCAAAGATTAGTTATAAAGACACTGAGCTTCTACTT 7141
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QY 2370 AAGCTAGCTGCCATGCTATGAGCAGCGCCTATAAAGAGACTTACGTGGTAAAAAATGAAGT 2429
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QY 2430 CTCCTGCCACAGCCACATTAGTGAACCTTAGAAGCAGAGACTCTGTGAGATTAATCGATGT 2489
DB 7262 CTCCTGCCACAGCCACATTAGTGAACCTTAGAAGCAGAGACTCTGTGAGATTAATCAATGT 7321
QY 2490 TTGTGTTTAAAGTTGCTCAGTTTGGTCTAACTTGTATGAGCAATAGATAAATAA 2549
DB 7322 TTGTGTTTAAAGTTGCTCAGTTTGGTCTAACTTGTATGAGCAATAGATAAATAA 7381
QY 2550 TGCAGAGAAAGAGA 2563
DB 7382 TGCAGAGAAAGAGA 7395
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## RESULT 13

US-09-417-455-7

; Sequence 7, Application US/09417455

; Patent No. 6294655

; GENERAL INFORMATION:

; APPLICANT: Ford, John

; APPLICANT: Face, Ann

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; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36328
; CURRENT APPLICATION NUMBER: US/09/417,455
; CURRENT FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 09/348,942
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: PCT/US99/04291
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/287,210
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/251,370
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 09/127,698
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 09/079,909
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/055,010
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 5751
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(5751)
; OTHER INFORMATION: n = A,T,C or G
US-09-417-455-7
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Query Match 63.1%; Score 1616.6; DB 3; Length 5751;

Best Local Similarity 98.9%; Pred. No. 0;

Matches 1663; Conservative 5; Mismatches 9; Indels 4; Gaps 4;

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DB 4073 ACCGAGTGAACATCATGGAGCTCTATCTTGGTGCCAGGAATCCAGAGCTTCACCTTCT 4132
QY 331 ACCGCGGGACATCGGGGCTCACCTCCAGCTTCGAGTCGGCTCCCTACCCGGGCTGGTTCC 390
DB 4133 ACCGCGGGACATCGGGGCTCACCTCCAGCTTCGAGTCGGCTCCCTACCCGGGCTGGTTCC 4192
QY 391 TGTGACCGTGCCTGAAAGCCGATCAGCTGTCCAGACTCACCCAGCTTCCGAGAAATGGTG 450
DB 4193 TGTGACCGTGCCTGAAAGCCGATCAGCTGTCCAGACTCACCCAGCTTCCGAGAAATGGTG 4252
QY 451 GCTGGAATGCCCCATCAGACTTCTACTTCCAGCAGTGACTAGGAGCAAGTCCGCC 510
DB 4253 GCTGGAATGCCCCATCAGACTTCTACTTCCAGCAGTGACTAGGAGCAAGTCCGCC 4311
QY 511 CCAGAACTCCCTCGGCGCAGAGCCAGCTCGGGTGAGGGGTGAGTGGAGGAGACCCATGGCG 570
DB 4312 CCAGAACTCCCTCGGCGCAGAGCCAGCTCGGGTGAGGGGTGAGTGGAGGAGACCCATGGCG 4371
QY 571 GACAACTACTCTTTCTGCTCTCAGAACCCCGAGGCTGTGACTTTAGTGGGCACTGACCACT 630
DB 4372 GACAACTACTCTCTGCTCTCAGAACCCCGAGGCTGTGACTTTAGTGGGCACTGACCACT 4431
QY 631 TTGCTTCTGTTTCCAGTTTGCATAAATTCGAGATTGGAGCTCAGTCCAGGGTCCCTC 690
DB 4432 TTGCTTCTGTTTCCAGTTTGGATAAATTCGAGATTGGAGCTCAGTCCAGGGTCCCTC 4491
QY 691 CCCCACTGGATGGTGTACTGTCTGTGGAACTTTGTAAAAAACCATGTGGGGTAAAACTGGGA 750
DB 4492 CCCCACTGGATGGTGTACTGTCTGTGGAACTTTGTAAAAAACCATGTGGGGTAAAACTGGGA 4551
QY 751 ATAACATGAAAGATTTCTGTGGGGGTGGGGAGTGTCTGGGAATCATTTCTGCTT 810
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Db	5631	GGTAGACCTAAATTAAATATGACTGGTTTCTTGTATGAAGAGGAGGACAGAGACA	5690
Qy	1889	GAGGAGACGCGGGAAGACTATATAAGATGAAGGCAGAGATCGGAGTTTTCGAGCCACA	1948
Db	5691	GAGGAGACGCGGGAAGACTATATAAGATGAAGGCAGAGATCGGAGTTTTCGAGCCACA	5750
Qy	1949	A 1949	
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RESULT 14			
US-09-348-942-7			
; Sequence 7, Application US/09348942			
; Patent No. 6337072			
; GENERAL INFORMATION:			
; APPLICANT: John Ford			
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF			
; FILE REFERENCE: 28110/35801			
; CURRENT APPLICATION NUMBER: US/09/348,942			
; CURRENT FILING DATE: 1999-07-07			
; EARLIER APPLICATION NUMBER: PCT/US99/04291			
; EARLIER FILING DATE: 1999-04-05			
; EARLIER APPLICATION NUMBER: US 09/287,210			
; EARLIER FILING DATE: 1999-04-05			
; EARLIER APPLICATION NUMBER: US 09/251,370			
; EARLIER FILING DATE: 1999-02-17			
; EARLIER APPLICATION NUMBER: US 09/229,591			
; EARLIER FILING DATE: 1999-01-13			
; EARLIER APPLICATION NUMBER: US 09/127,698			
; EARLIER FILING DATE: 1998-07-31			
; EARLIER APPLICATION NUMBER: US 09/099,818			
; EARLIER FILING DATE: 1998-06-19			
; EARLIER APPLICATION NUMBER: US 09/082,364			
; EARLIER FILING DATE: 1998-05-20			
; EARLIER APPLICATION NUMBER: US 09/079,909			
; EARLIER FILING DATE: 1998-05-15			
; EARLIER APPLICATION NUMBER: US 09/055,010			
; EARLIER FILING DATE: 1998-04-03			
; NUMBER OF SEQ ID NOS: 30			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 7			
; LENGTH: 5751			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc feature			
; LOCATION: (1)..(5751)			
; OTHER INFORMATION: n = A,T,C or G			
US-09-348-942-7			
Query Match 63.1%; Score 1616.6; DB 3; Length 5751;			
Best Local Similarity 98.9%; Pred.No. 0;			
Matches 1663; Conservative 5; Mismatches 9; Indels 4; Gaps 4;			
Qy	271	AGCCAGTGAACATCATCGAGCTCTATCTTGGTGCCAAAGAAATCCAAAGAGTTTCACCTTCT	330
Db	4073	AGCCAGTGAACATCATCGAGCTCTATCTTGGTGCCAAAGAAATCCAAAGAGTTTCACCTTCT	4132
Qy	331	ACCGGCGGACATGCGGCTCACTCCAGCTTCGAGTCGCGTACCCGGGCTGTTTC	390
Db	4133	ACCGGCGGACATGCGGCTCACTCCAGCTTCGAGTCGCGTACCCGGGCTGTTTC	4192
Qy	391	TGTGCAAGTGCCTGAAGCGGATCAGCCTGTCCAGCTCACCCAGCTTCCCGAATGGTG	450
Db	4193	TGTGCAAGTGCCTGAAGCGGATCAGCCTGTCCAGCTCACCCAGCTTCCCGAATGGTG	4252
Qy	451	GCTGGAAATGCCCCATCACAGACTTCTACTTCCAGCAGTGTGACTAGGGCAACGTGCCCC	510
Db	4253	GCTGGAAATGCCCCATCACAGACTTCTACTTCCAGCAGTGTGACTAGGGCAACGTG-CCC	4311
Qy	511	CCGAGAATCTCCCTGGGCGAGCCAGCTCGGGTGAGGTGAGGAGAGACCCATGGCG	570



Matches 1663; Conservative 5; Mismatches 9; Indels 4; Gaps 4;			
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DB	4133	ACGGGGGACATGGGCTCACCTCAGCTTCGAGTCCGGCTGCTACCCGGGCTGGTTCC	4192
QY	391	TGTGACCGGTGCTGAAGCCGATCAGCTGTGAGCTCACCCAGCTTCCCGAGAAATGGTG	450
DB	4193	TGTGACCGGTGCTGAAGCCGATCAGCTGTGAGCTCACCCAGCTTCCCGAGAAATGGTG	4252
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DB	4253	GCTGGAATGCCCCCATCACAGACTTCTACTTCCAGCAGTGTGACTAGGSCAAAGTCCGCC	4311
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DB	4312	CCAGAACTCCCTGGGACAGCCAGCTCGGCTGAGGGGTGAGTGGAGGAGACCCATGGCG	4371
QY	571	GACAACTCACTTTCTGTCTCTCAGGACCCCGAGTCTGACTTAGTGGGCACCTGACCACT	630
DB	4372	GACAACTCACTTTCTGTCTCTCAGGACCCCGAGTCTGACTTAGTGGGCACCTGACCACT	4431
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DB	4432	TTGTCTTCTGGTTCCAGTTTGCATAAAATCTGAGATTTGGAGCTCAGTCCAGGGTCTTC	4491
QY	691	CCCCACTGATGGTGTCTACTGTGTGGAACTTGTGTAAGAAACCATGTGGGGTAAACTGGGA	750
DB	4492	CCCCACTGATGGTGTCTACTGTGTGGAACTTGTGTAAGAAACCATGTGGGGTAAACTGGGA	4551
QY	751	ATAACATGAAGATTTCTGTGGGGTGGGGTGGGGAGTGTGGGAATCATTTCTGTCTT	810
DB	4552	ATAACATGAAGATTTCTGTGGGGTGGGGTGGGGAGTGTGGGAATCATTTCTGTCTT	4611
QY	811	AATGGTAACTGACAAAGTGTATACCTGAGCCCGGAGCCCAACCCATCCCGAGTTCAGCCT	870
DB	4612	AATGGTAACTGACAAAGTGTATACCTGAGCCCGGAGCCCAACCCATCCCGAGTTCAGCCT	4671
QY	871	TATAGGTCAGTAGTCTCCACATGAGTCTCTCACTCACCACTGTGAGGAGAGGGAG	930
DB	4672	TATAGGTCAGTAGTCTCCACATGAGTCTCTCACTCACCACTGTGAGGAGAGGGAG	4731
QY	931	GTGGTCATAGAGTCAGGGATCTATGGCCCTTGSCCCAGCCCAACCCCTTCCCTTT-ATC	989
DB	4732	GTGGTCATAGAGTCAGGGATCTATGGCCCTTGSCCCAGCCCAACCCCTTCCCTTTAATC	4791
QY	990	CTGCCACTGTCTATGCTACCTTTCTCTATCTCTTCCCTCATCATCTTGTGGGCATGA	1049
DB	4792	CTGCCACTGTCTATGCTACCTTTCTCTATCTCTTCCCTCATCATCTTGTGTGGGCATGA	4851
QY	1050	GGAGTGGTGTGTGAGAGAAATGGTTCGAGCTCAGAGAGATAAAGATAAGTAGGGTAT	1109
DB	4852	GGAGTGGTGTGTGAGAGAAATGGTTCGAGCTCAGAGAGATAAAGATAAGTAGGGTAT	4911
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DB	4912	GCTGATCTCTTTTAAAAAACCAGATACAAATCAAAATCCAGATGCTGGTCTCTATTTC	4971
QY	1169	CCATGAAAAGTGTCTATGACATATTGAGAGACCTTACTTACAAAGTGGCATATATTGCA	1228
DB	4972	CCATGAAAAGTGTCTATGACATATTGAGAGACCTTACTTACAAAGTGGCATATATTGCA	5031
QY	1229	ATTATATTTTAAATTAAGATACCTATTATATATTCTTTTATAGAAAAAAGTCTGGAAGA	1288
DB	5032	ATTATATTTTAAATTAAGATACCTATTATATATTCTTTTATAGAAAAAAGTCTGGAAGA	5091
QY	1289	GTTTACTTCAATGTAGCAATGTACGGGTGGGCGAGTATAGGTGATTTTCTTTTAATT	1348
DB	5092	GTTTACTTCAATGTAGCAATGTACGGGTGGGCGAGTATAGGTGATTTTCTTTTAATT	5151

1349 CTGTTAAATTTATCTGTATTTTCTTAATTTTCTACAATGAAGATGAATTCCTTGTATAAAA 1408  
1512 CTGTTAAATTTATCTGTATTTTCTTAATTTTCTACAATGAAGATGAATTCCTTGTATAAAA 5211  
1409 ATAAGAAAGAAATTAATCTTCTGAGGTAAAGCAGAGAGACATCATCTCTGATTTGCTCAG 1468  
5212 ATAAGAAAGAAATTAATCTTCTGAGGTAAAGCAGAGAGACATCATCTCTGATKG-CCTCAG 5270  
1469 CTTCAAATTTCCCCAGAGATAAATTCAAATTTGAATCGAGCTCTGCTCTGTTGGTTGTA 1528  
5271 CTTCCACTTTCCCCAGAGATAAATTCAAATTTGAATCGAGCTCTGCTCTGTTGGTTGTA 5330  
1529 GTAGTGATCAGAAACAGATCTCAGAAAGCCACTGAGAGAGAGGCTGTGAGTTTGT 1588  
5331 GTAGTGATCAGAAACAGATCTCAGAAAGCCACTGAGAGAGAGGCTGTGATGAGTTGT 5390  
1589 GTGGCTGGAACTCTCTGGGTAAAGAACTTAAAGAAACAAATCATCTGGTAATTTCTTCT 1648  
5391 GTGGCTGGAACTCTCTGGGTAAAGAACTTAAAGAAACAAATCATCTGGTAATTTCTTCT 5450  
1649 AGAAGGATCACAGCCCTGGGATTTCAAGGCAATGGATCCAGTCTCTAAGAAAGGCTGCTG 1708  
5451 AGAAGGATCACAGCCCTGGGATTTCAAGGCAATGGATCCAGTCTCTAAGAAAGGCTGCTG 5510  
1709 TACTGTTGAAATTTGTTGCCCTCAAAATTCACATCTCTTCTGGAATCTCAGTCTGTGAGT 1768  
5511 TACTGTTGAAATTTGTTGCCCTCAAAATTCACATCTCTTCTGGAATCTCAGTCTGTGAGT 5570  
1769 TTAATTTGGAGATAAGGTCTCTGACATGTAGTTAGTAAAGCAAGGTCTGCTGGATGAA 1828  
5571 TTAATTTGGAGATAAGGTCTCTGACATGTAGTTAGTAAAGCAAGGTCTGCTGGATGAA 5630  
1829 GGTAGACCTAAATTCAAATATGACTGTTTCTTGTATGAAAAGAGAGAGACACAGAGACA 1888  
5631 GGTAGACCTAAATTCAAATATGACTGTTTCTTGTATGAAAAGAGAGAGACACAGAGACA 5690  
1889 GAGGAGACCGGGGAGAGACTATGTAAAGATGAAGCAGAGATCGGAGTTTTGCAGCCACA 1948  
5691 GAGGAGACCGGGGAGAGACTATGTAAAGATGAAGCAGAGATCGGAGTTTTGCAGCCACA 5750  
1949 A 1949  
5751 A 5751

Search completed: March 13, 2005, 18:22:11  
Job time : 495.866 secs



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OM nucleic - nucleic search, using sw model

Run on: March 13, 2005, 10:45:20 ; Search time 22.9062 Seconds  
(without alignments)  
10854.228 Million cell updates/sec

Title: US-09-617-720A-3

Perfect score: 42

Sequence: 1 aagggaaggaggagagga.....gagtgaggaaggagtgaaa 42

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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11: Geneseqn2003ds:\*  
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13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	42	5	Aaf27923 Human IL-
2	42	100.0	73	5	Aaf27926 Interleuk
3	42	100.0	6540	5	Aaf27950 Interleuk
4	42	100.0	7605	2	Aaz30053 DNA encod
5	42	100.0	7605	4	Aaf31356 Extension
6	42	100.0	7605	8	Abz77451 Extended
7	33	78.6	446	2	Aaq95200 Simple ta
8	32	76.2	110000	13	Continuation (7 of
9	31.4	74.8	4579	12	Adj75968 Marker ge
10	31.4	74.8	165156	13	Adg36459 Human aut
11	31.4	74.8	335199	10	Adc24703 Human wil
12	30.8	73.3	52661	9	Ada02876 Human DPT
13	30.8	73.3	52661	10	Adb72614 Human DPT
14	30.8	73.3	52661	10	Adc85355 Mouse Dpt
15	30.8	73.3	52661	12	Adm74471 Human car
16	30.8	73.3	59588	10	Adc87426 Human GPC
17	30.8	73.3	74822	6	Abt10752 Human bre
18	30.4	72.4	3973	6	Ab132170 Human inm
19	29.8	71.0	496	6	Abk88541 Human cho
20	29.8	71.0	867	3	Aaz98056 Human sec

C 21	29.8	71.0	867	4	AAD11669	Ad11669 Human sec
C 22	29.8	71.0	867	6	ABK69765	Abk69765 Human sec
C 23	29.8	71.0	867	8	ADA39774	Ada39774 Human sec
C 24	29.8	71.0	867	8	ACC50425	Acc50425 Human sec
C 25	29.8	71.0	867	8	ABZ71239	Abz71239 Human sec
C 26	29.8	71.0	867	9	ADB91132	Adb91132 Human sec
C 27	29.8	71.0	867	10	ADC73483	Adc73483 Human sec
C 28	29.8	71.0	867	10	ADA55964	Ada55964 Gene enco
C 29	29.8	71.0	2777	8	AH332536	Aah332536 Human sec
C 30	29.8	71.0	2777	4	ADA39721	Ada39721 Human sec
C 31	29.8	71.0	2777	8	ACC50392	Acc50392 Human sec
C 32	29.8	71.0	2777	10	ADA55915	Ada55915 Gene enco
C 33	29.8	71.0	12141	4	Aaf62854	Aaf62854 Mouse PEP
C 34	29.8	71.0	12141	12	ADP18732	Adp18732 Mouse lip
C 35	29.8	71.0	21777	4	AAK74096	Aak74096 Human imm
C 36	29.8	71.0	28729	11	ACN43928	Acn43928 Mouse gen
C 37	29.8	71.0	41966	11	ACN45050	Acn45050 Human gen
C 38	29.8	71.0	57082	12	ADP84151	Adp84151 Human CAL
C 39	29.8	71.0	96589	9	AAL57700	Aal57700 Mouse pro
C 40	29.8	71.0	96592	9	ADA02669	Ada02669 Mouse Prl
C 41	29.8	71.0	96592	10	ADB72407	Adb72407 Mouse Prl
C 42	29.8	71.0	96592	10	ADB72407	Adb72407 Mouse Prl
C 43	29.8	71.0	97658	8	ABO83210_3	Ab083210_3 of
C 44	29.8	71.0	110000	13	ABD32594_3	Continuation (4 of
C 45	29.8	71.0	117962	8	AAD54480	Ad54480 Human CIP

#### ALIGNMENTS

#### RESULT 1

AAF27923

ID AAF27923 standard; cDNA; 42 BP.

XX

AC AAF27923;

XX

DT 08-MAY-2001 (first entry)

XX

DE Human IL-IL1 coding sequence 5' end #2.

XX

KW Human; IL-IL1; interleukin-1 locus; IL-1beta; IL-1receptor; psoriasis;  
chromosome 2q13; inflammatory disease; heart disease; Graves' disease;  
rheumatoid arthritis; inflammatory bowel disorder; diabetes; cancer;  
osteoporosis; systemic lupus erythematosus; ss.

XX

OS Homo sapiens.

XX

PN WO200105974-A2.

XX

PD 25-JAN-2001.

XX

PF 17-JUL-2000; 2000WO-US019508.

XX

PR 16-JUL-1999; 99US-0144298P.

XX

PA (INTE-) INTERLEUKIN GENETICS INC.

XX

PI Nicklin M, Barton J;

XX

DR WPI; 2001-091974/10.

XX

PT Nucleic acids encoding human and murine interleukin-IL1 polypeptides  
useful for controlling inflammatory processes.

XX

PS Claim 21; Fig 1; 150pp; English.

XX

The present invention provides the protein and coding sequences of the  
human and murine interleukin-IL1 (IL-IL1) proteins. The IL-IL1 gene is  
located between the IL-1beta and IL-1receptor genes at human chromosome  
2q13. The sequences are useful in the diagnosis, prevention and treatment  
of heart disease, cancer and inflammatory diseases such as rheumatoid  
arthritis, systemic lupus erythematosus, inflammatory bowel disorder,  
diabetes, psoriasis, osteoporosis, lichen sclerosis, ulcerative colitis,



KW	intrauterine infection; nutritional activity;
KW	hematopoiesis regulating activity; tissue growth activity;
KW	activin activity; inhibin activity; chemotactic activity;
KW	chemokinetic activity; hemostatic activity; thrombolytic activity;
KW	anti-inflammatory activity; ss.
OS	Homo sapiens.
XX	
PN	WO9951744-A2.
XX	
PD	14-OCT-1999.
XX	
PF	05-APR-1999; 99WO-US004291.
XX	
PR	03-APR-1998; 98US-00055010.
PR	15-MAY-1998; 98US-00079909.
PR	20-MAY-1998; 98US-00082364.
PR	19-JUN-1998; 98US-00099818.
PR	31-JUL-1998; 98US-00127698.
PR	13-JAN-1999; 99US-00229591.
PR	17-FEB-1999; 99US-00251370.
XX	
PA	(HYSB-) HYSEQ INC.
XX	
PI	Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
PI	Leshkowitz D, Kita D, Ford J, Pace A, Alfenito M;
XX	
DR	WPI; 1999-611042/52.
XX	
PT	New isolated interleukin-1 receptor binding polypeptides, used to treat
PT	e.g. sepsis, shock, arthritis, pancreatitis, graft-versus-host disease,
PT	inflammatory disease, autoimmune disease or proliferative disease.
XX	
PS	Disclosure; Fig 10A-C; 123pp; English.
XX	
CC	The present sequence encodes a human interleukin-1 (IL-1) receptor
CC	antagonist. It is an extension of AAZ30052. The encoded polypeptide is
CC	capable of binding IL-1 receptors (IL-1Rs). The polynucleotides and
CC	polypeptides can be used for the prevention or treatment of disorders
CC	involving sepsis, acute pancreatitis, endotoxin shock, cytokine induced
CC	shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic
CC	cell damage from diabetes mellitus type 1, graft versus host disease,
CC	inflammatory bowel disease, inflammation associated with pulmonary
CC	disease, other autoimmune disease or inflammatory disease, an
CC	antiproliferative agent such as for acute or chronic myelogenous leukemia
CC	or in the prevention of premature labor secondary to intrauterine
CC	infections. They can also exhibit activities such as e.g. nutritional
CC	activity, cytokine and cell proliferation/differentiation activity,
CC	immune stimulating or suppressing activity, hematopoiesis regulating
CC	activity, tissue growth activity, activin/inhibin activity, chemotactic/
CC	chemokinetic activity, hemostatic and thrombolytic activity, receptor/
CC	ligand activity, and anti-inflammatory activity. The products can also be
CC	used for detection, diagnosis and drug screening
XX	
SQ	Sequence 7605 BP; 2081 A; 1647 C; 1865 G; 2007 T; 0 U; 5 Other;
	Query Match 100.0%; Score 42; DB 2; Length 7605;
	Best Local Similarity 100.0%; Pred. No. 0.0015;
	Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 AAGGAAGCGGGGAGGAGGAGGAGTGAAGGAAGGAGTGA 42
Db	1338 AAGGAGGAGGAGGAGGAGGAGGAGTGAAGGAAGGAGTGA 1379
RESULT 5	
AAF31356	
ID	AAF31356 standard; DNA; 7605 BP.
XX	
AC	AAF31356;
XX	
DT	05-APR-2001 (first entry)
XX	





PF 18-MAR-2004; 2004WO-US008461.

intron  
109002: .20586

## III

FT exon 205869. .205928  
FT /tag= e  
FT /number= 2b  
FT intron 205929. .209525  
FT /tag= f  
FT /number= 2b  
FT exon 209526. .209679  
FT /tag= g  
FT /number= 3  
FT intron 209680. .235027  
FT /tag= h  
FT /number= 3  
FT exon 235028. .235139  
FT /tag= i  
FT /number= 3b  
FT intron 235140. .238089  
FT /tag= j  
FT /number= 3b  
FT exon 238090. .238212  
FT /tag= k  
FT /number= 3t  
FT intron 238213. .310596  
FT /tag= l  
FT /number= 3t  
FT exon 310597. .310783  
FT /tag= m  
FT /number= 4  
FT intron 310784. .316138  
FT /tag= n  
FT /number= 4  
FT exon 316139. .316929  
FT /tag= o  
FT /number= 5  
FT intron 316930. .326821  
FT /tag= p  
FT /number= 5  
FT exon 326822. .330136  
FT /tag= q  
FT /number= 6  
XX WO2003045998-A2.  
XX  
XX 05-JUN-2003.  
XX  
XX 02-DEC-2002; 2002WO-FR004134.  
XX  
XX 30-NOV-2001; 2001CA-02364106.  
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
XX (INSP ) INST PASTEUR.  
XX (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.  
XX Bourgeron T, Jamain S, Quach H, Betancur C, Leboyer M;  
XX Gillberg C;  
XX WPI; 2003-493399/46.  
XX  
XX New nucleic acid encoding mutant protein involved in synaptogenesis,  
XX useful for treatment and diagnosis of e.g. autism, Asperger syndrome, and  
XX schizophrenia.  
XX  
XX Claim 10; SEQ ID NO 4; 416pp; French.  
XX  
XX The invention relates to an isolated or purified polynucleotide encoding  
XX a polypeptide (the wild-type form of which is involved in synaptogenesis)  
XX that includes at least one mutation associated with development of  
XX neurological disease and/or a predisposition to development of mental  
XX disorders or psychiatric illness. The polypeptide are used to screen for  
XX agents that modulate their activity. Also nucleic acid, polypeptide,  
XX polypeptide-specific antibodies, vectors containing he nucleic acid and  
XX host cells containing the vector, are useful as pharmaceuticals for  
XX treating mental and neurological disorders, specifically autism, Asperger  
XX syndrome, schizophrenia and attention deficit hyperactivity disorder. CC

CC wild-type forms of the nucleic acid and polypeptide can be used  
CC similarly. Also detecting mutations in the nucleic acid and polypeptide,  
CC or measuring activity of the polypeptide, can be used to detect  
CC biochemical disorders that affect formation of synapses and to diagnose  
CC mental disease. This sequence corresponds to the genomic sequence of the  
CC human wild type HNLAY gene.  
XX  
SQ Sequence 335199 BP; 98958 A; 63589 C; 65677 G; 106975 T; 0 U; 0 Other;  
Query Match 74.8%; Score 31.4; DB 10; Length 335199;  
Best Local Similarity 85.4%; Pred. No. 3.1;  
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 AAGGAAGGAGGAGGAGGAGGAGGTGAAGGAGGAGGTGAA 41  
Db 299390 AGGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA 299350  
RESULT 12  
ADA02876  
ID ADA02876 standard; DNA; 52661 BP.  
XX  
AC ADA02876;  
XX  
DT 06-NOV-2003 (first entry)  
XX  
DE Human DPT carcinoma associated gene, SEQ ID NO:1394.  
XX  
KW Human; carcinoma associated; oncogene; carcinoma; cancer; breast;  
KW prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;  
KW gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO2003057146-A2.  
XX  
PD 17-JUL-2003.  
XX  
PF 26-DEC-2002; 2002WO-US041414.  
XX  
PR 26-DEC-2001; 2001US-00035832.  
XX  
PA (SAGR-) SAGRES DISCOVERY.  
XX  
PI Morris DW;  
XX  
DR WPI; 2003-587068/55.  
XX  
PT New recombinant nucleic acid encoding carcinoma associated protein,  
PT useful for preparing compositions for treating carcinomas.  
XX  
PS Claim 1; SEQ ID NO 1394; 245pp; English.  
XX  
XX The invention relates to recombinant carcinoma associated (CA) nucleic  
XX acid sequences from mouse and human (ADA01482-ADA03094), and to  
XX recombinant carcinoma associated proteins (CAP) encoded by them. The  
XX invention also encompasses expression vectors and host cells comprising a  
XX CA nucleic acid, a polypeptide (especially an antibody) that specifically  
XX binds to the protein, and a biochip comprising CA nucleic acid or  
XX fragments thereof. The sequences of the invention were identified using  
XX oncogenic retroviruses, which insert into the genome of the host organism  
XX at random. Many of these do not carry transduced host oncogenes or  
XX pathogenic trans-acting viral genes, meaning that cancer incidence is a  
XX direct consequence of the effects of proviral integration into host  
XX protooncogenes. The CA nucleic acid sequences can be used to diagnose  
XX carcinoma (especially breast cancer, prostate cancer, lymphoma or  
XX leukaemia) or a propensity to carcinoma by determination of the sequence  
XX of a CA gene, or by determination of CA gene expression in particular  
XX tissues. CA nucleic acids, proteins and antibodies are also useful as  
XX therapeutic agents and in screening and evaluating drug candidates. The  
XX present sequence represents a specifically claimed human CA nucleic acid  
XX sequence of the invention. Note: The complete sequence data for this  
XX patent did not form part of the printed specification, but was obtained CC

CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX

SQ Sequence 52661 BP; 15800 A; 11001 C; 11082 G; 14778 T; 0 U; 0 Other;  
Query Match 73.3%; Score 30.8; DB 9; Length 52661;  
Best Local Similarity 83.3%; Pred. No. 4.1;  
Matches 35; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 AAGGAAGGAGGAGAAGGGAAGGAGTGAAGGAGGAGTGAAA 42  
| | | | | | | | | | | | | | | | | | | | |  
Db 13858 AGGGAGGAGGAGGAGGAGGATTGAAGGAAGGAGAAA 13899

RESULT 13  
ADB72614  
ID ADB72614 standard; DNA; 52661 BP.  
XX  
AC ADB72614;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Human DPT gene.  
XX  
KW human; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;  
KW cancer; neoplasm; adenocarcinoma; sarcoma; gene.  
XX  
OS Homo sapiens.  
XX  
PN WO2003008583-A2.  
XX  
PP 30-JAN-2003.  
XX  
XX 26-DEC-2001; 2001WO-US051291.  
XX  
PR 02-MAR-2001; 2001US-00798586.  
PR 23-OCT-2001; 2001US-00004113.  
PR 08-NOV-2001; 2001US-00052482.  
PR 30-NOV-2001; 2001US-00997722.  
PR 20-DEC-2001; 2001US-00034650.  
XX  
PA (SAGR-) SAGES DISCOVERY.  
XX  
PI Morris DW, Engelhard EK;  
XX  
PS WPI; 2003-239337/23.  
XX  
DR New recombinant nucleic acid, useful for treating carcinomas, lymphomas,  
PT cancers, neoplasm, adenocarcinoma, or sarcomas.  
XX  
PS Claim 1; SEQ ID NO 442; 2304pp; English.

CC The invention relates to a novel recombinant nucleic acid comprising a  
CC nucleotide sequence selected from any of the 660 sequences fully defined  
CC in the specification. A polynucleotide of the invention has cytosstatic  
CC activity, and may have a use in gene therapy, or in a vaccine. The  
CC recombinant nucleic acids and polypeptides are useful for treating  
CC carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and  
CC sarcomas. The present sequence represents a human gene of the invention.

XX  
SQ Sequence 52661 BP; 15800 A; 11001 C; 11082 G; 14778 T; 0 U; 0 Other;  
Query Match 73.3%; Score 30.8; DB 10; Length 52661;  
Best Local Similarity 83.3%; Pred. No. 4.1;  
Matches 35; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 AAGGAAGGAGGAGAAGGGAAGGAGTGAAGGAGGAGTGAAA 42  
| | | | | | | | | | | | | | | | | | | | |  
Db 13858 AGGGAGGAGGAGGAGGAGGATTGAAGGAAGGAGAAA 13899

RESULT 14  
ADC85355



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OM nucleic - nucleic search, using sw model

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10959.418 Million cell updates/sec

Title: US-09-617-720A-1

Perfect score: 2563

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb\_htg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_to.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2563	100.0	2563	6	AX080389 Sequence
2	2539	99.1	2604	9	AJ242738 Homo sapi
3	2539	99.1	2613	9	AJ242737 Homo sapi
4	2514.2	98.1	2598	6	AX092420 Sequence
5	2514.2	98.1	2598	6	AX454730 Sequence
6	2514.2	98.1	2598	6	AX491208 Sequence
7	2514.2	98.1	2598	9	AY359117 Homo sapi
8	2512	98.0	2692	9	BC024747 Homo sapi
9	2504.2	97.7	2701	6	C0722801 Sequence
10	2488.4	97.1	2648	6	BD211435 A novel i
11	2488.4	97.1	2648	6	AR181995 Sequence
12	2488.4	97.1	2648	6	AR221129 Sequence
13	2488.4	97.1	2648	6	AR302957 Sequence
14	2488.4	97.1	2648	6	AX069309 Sequence
15	2488.4	97.1	2720	9	AF186094 Homo sapi
16	2235.6	87.2	6540	6	AX080431 Sequence
17	2235.6	87.2	6540	9	AJ271338 Homo sapi
18	2229.2	87.0	197308	9	AC016724 Homo sapi
19	2220.4	86.6	7604	9	AF216693 Homo sapi

20	2220.4	86.6	7605	6	BD211437	BD211437 A novel i
21	2220.4	86.6	7605	6	AR181997	AR181997 Sequence
22	2220.4	86.6	7605	6	AR221131	AR221131 Sequence
23	2220.4	86.6	7605	6	AR302959	AR302959 Sequence
24	2220.4	86.6	7605	6	AX069311	AX069311 Sequence
25	1835	71.6	1866	6	BD157091	BD157091 Primer fo
26	1835	71.6	1866	6	AX878219	AX878219 Sequence
27	1835	71.6	1866	9	AK002125	AK002125 Homo sapi
28	1616.6	63.1	5751	6	BD211436	BD211436 A novel i
29	1616.6	63.1	5751	6	AR181996	AR181996 Sequence
30	1616.6	63.1	5751	6	AR221130	AR221130 Sequence
31	1616.6	63.1	5751	6	AR302958	AR302958 Sequence
32	1616.6	63.1	5751	6	AX069310	AX069310 Sequence
33	1241.8	48.5	1288	9	AF201830	AF201830 Homo sapi
34	1195.2	46.6	1282	6	BD211434	BD211434 A novel i
35	1195.2	46.6	1282	6	AR181994	AR181994 Sequence
36	1195.2	46.6	1282	6	AR221128	AR221128 Sequence
37	1195.2	46.6	1282	6	AR302956	AR302956 Sequence
38	1195.2	46.6	1282	6	AX069307	AX069307 Sequence
39	950	37.1	1025	6	AX207818	AX207818 Sequence
40	941.2	36.7	985	6	BD211433	BD211433 A novel i
41	941.2	36.7	985	6	AR181993	AR181993 Sequence
42	941.2	36.7	985	6	AR221127	AR221127 Sequence
43	941.2	36.7	985	6	AR302955	AR302955 Sequence
44	941.2	36.7	985	6	AX069305	AX069305 Sequence
45	527.8	20.6	555	6	BD149991	BD149991 Primer fo

ALIGNMENTS

RESULT 1	AX080389	Sequence 1 from Patent WO0105974.	2563 bp	DNA	linear	PAT 22-FEB-2001
LOCUS	AX080389	Sequence 1 from Patent WO0105974.	2563 bp	DNA	linear	PAT 22-FEB-2001
DEFINITION	AX080389	Sequence 1 from Patent WO0105974.	2563 bp	DNA	linear	PAT 22-FEB-2001
ACCESSION	AX080389	Sequence 1 from Patent WO0105974.	2563 bp	DNA	linear	PAT 22-FEB-2001
VERSION	AX080389.1	GI:13159840	2563 bp	DNA	linear	PAT 22-FEB-2001
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REFERENCE	AX080389.1	GI:13159840	2563 bp	DNA	linear	PAT 22-FEB-2001
AUTHORS	AX080389.1	GI:13159840	2563 bp	DNA	linear	PAT 22-FEB-2001
TITLE	AX080389.1	GI:13159840	2563 bp	DNA	linear	PAT 22-FEB-2001
JOURNAL	AX080389.1	GI:13159840	2563 bp	DNA	linear	PAT 22-FEB-2001
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Qy	2461	AAGCAGAGACTCTGTGAGATAATCGATGTTGTTGTTGTTTAAAGTTCCTCAGTTTTGTTGTTCTA	2520		120	CTGCATGCAGGGAAGGTCAATTAAGGTGAAGAGATCAGCGTGGTCCCAATCGSTGGCTG	179
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Qy	2521	ACTTGTATTGACGCAATAGATAAATAATATGACAGAGAAGAGA	2563		180	GATGCAGCTGTCCTCCCGTCACTCCTGGGTGTCAGGGTGAAGCCAGTGCCTGTCTATGT	239
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RESULT 2							
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DEFINITION	Homo sapiens mRNA for interleukin-1-like protein 1 (IL1L1 gene)						
ACCESSION	AJ242738						
VERSION	AJ242738.1	GI:6165335					
KEYWORDS	IL1L1 gene; interleukin-1-like protein 1.						
SOURCE	Homo sapiens (human)						
ORGANISM	Homo sapiens						
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
REFERENCE	1						
AUTHORS	Barton, J.L., Herbst, R., Bosio, D., Higgins, L. and Nicklin, M.J.						
TITLE	A tissue specific IL-1 receptor antagonist homolog from the IL-1						
	cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities						
JOURNAL	Eur. J. Immunol. 30 (11), 3299-3308 (2000)						
MEDLINE	20545212						
PUBMED	11093146						
REFERENCE	2 (bases 1 to 2504)						
AUTHORS	Nicklin, M.J.						
TITLE	Direct Submission						
JOURNAL	Submitted (09-JUN-1999) Nicklin M.J., Division of Molecular and						
	Genetic Medicine, University of Sheffield, Royal Hallamshire						
	Hospital, Glossop Road, Sheffield, S10 2JF, UNITED KINGDOM						
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ORIGIN							
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Best Local Similarity	99.9%; Pred. No. 0;						
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Db	43	AGGGAGTCTACCTCTGGAAAGCTCAAGATGGTCTGAGTGGGGCGCTGCTTCGCA	102		1123	AGCTCAGAAGATAAAGATAGTAGGGTATGCTGATCTCTTTTAAAAACCCAAAGATACA	1182
Qy	60	ATGAAGGACTCGGCATTGAAGTGTCTTTATCTGCATAATAACCACTTCTAGCTGAGGG	119		1140	ATCAAAATCCCAGATGCTGCTCTATTCCCATGAAAAAGTCTCATGATATTGAGAA	1199





/evidence=experimental

## ORIGIN

Query Match	99.1%;	Score 2539;	DB 9;	Length 2613;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 2561;	Conservative 0;	Mismatches 0;	Indels 2;	Gaps 2;

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Qy	60	ATGAAGACTCGGCATTGGAAGTCTTTATCTGCAATAATAAACAGCTTCTAGCTTGGAGGG	119
Db	112	ATGAAGACTCGGCATTGGAAGTCTTTATCTGCAATAATAACCAAGCTTCTAGCTGGAGGG	171
Qy	120	CTGCATCGAGGAGGTCATTAAAGGTGAAGAGATCAGCGTGGTCCCCCAATCGGTGCGTG	179
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Qy	420	GTCAAGCTCAACCAGTTCCTCGAGAAATGGTGGTGGAAATGCCCAATCAAGAGCTTCTTAC	479
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Qy	480	TTCCAGAGTGTGACTAGGCGACAGTGCCTCCCGGAGAACTCCCTGGGCGAGCCAGCTCG	539
Db	532	TTCCAGAGTGTGACTAGGCGCAAGTGCCTCCCGGAGAACTCCCTGGGCGAGCCAGCTCG	591
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Db	592	GGTGAGGGGTGAGTGGAGGAGACCCATGGCGGACAATCACTCTTTCTGTCTCTCAGGACCC	651
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ACCESSION AX454730  
VERSION AX454730.1 GI:21713989  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I. and Ye, W.

TITLE Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis  
JOURNAL Patent: WO 0208284-A 315 31-JAN-2002; Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard, Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ; Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US) ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ; Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William I. (US)

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Qy 121 TGCATGCGGGAAGGTCAATAAGGTGAAGAGATCAGCGTGGTCCCAATCGGTGGCTGG 180  
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REFERENCE	1 (bases 1 to 2598)
AUTHORS	Clark,H.P., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Denel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seahagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.
TITLE	The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins:
JOURNAL	A Bioinformatics Assessment
PUBMED	Genome Res. 13 (10), 2265-2270 (2003)
REFERENCE	2 (bases 1 to 2598)
AUTHORS	Clark,H.P.
TITLE	Direct Submission
JOURNAL	Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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LOCUS	BC024747	2692 bp	mRNA linear PRI 30-JUN-2004
DEFINITION	Homo sapiens interleukin 1 family, member 5 (delta), transcript variant 2, mRNA (cDNA clone MGC:29840 IMAGE:4996939), complete cds.		
ACCESSION	BC024747		
VERSION	BC024747.1	GI:19353229	
KEYWORDS	MGC.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 2692)		
AUTHORS	Strausberg, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., R.A., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzyzinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
PUBMED	12477932		
REFERENCE	2 (bases 1 to 2692)		
AUTHORS	Strausberg, R.		
TITLE	Direct Submission		
JOURNAL	Submitted (01-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>		
COMMENT	Contact: MGC help desk Email: <a href="mailto:cgaps-x@mail.nih.gov">cgaps-x@mail.nih.gov</a> Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: <a href="http://www.hgsc.bcm.tmc.edu/cdna/">http://www.hgsc.bcm.tmc.edu/cdna/</a> Contact: <a href="mailto:amg@bcm.tmc.edu">amg@bcm.tmc.edu</a> Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.		
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Series: IRAK Plate: 42 Row: k Column: 16 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27894309. Location/Qualifiers 1. .2692 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MGC:29840 IMAGE:4996939" /tissue_type="Placenta, Choriocarcinoma" /clone_lib="NIH_MGC_10"		
source			
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CDS			
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Db 2172 CTCTGCTGAACCTTAATCTCAGACTTCCAGCCTCCTGACGAGAAAGATAAATTCG 2231  
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RESULT 10  
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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
OS Homo sapiens (human)  
PN JP 2002510492-A/4  
PD 09-APR-2002  
PF 05-APR-1999 JP 2000542457  
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PI JOHN FORD,ANN PACE  
PC C12N15/09,A61K38/00,C07K14/52,C07K14/545,C07K16/24,C12N1/15,  
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RESULT 11

AR181995 LOCUS AR181995 2648 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 6 from patent US 6337072.  
ACCESSION AR181995  
VERSION AR181995.1 GI:20224911

KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2648)  
AUTHORS Ford, J. and Pace, A.  
TITLE Interleukin-1 receptor antagonist and recombinant production thereof  
JOURNAL Patent: US 6337072-A 6 08-JAN-2002;  
FEATURES Location/Qualifiers  
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ORIGIN

Query Match 97.1%; Score 2488.4; DB 6; Length 2648;  
Best Local Similarity 99.4%; Pred. No. 0;  
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Qy 1 AGGGAGTCTACACCTCTGGAGCTCAAGATGGTCTCAGTGGGGCGCTGCTCCGAA 60  
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DEFINITION Sequence 6 from patent US 6541623.  
ACCESSION AR302957  
VERSION AR302957.1 GI:31691557  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

Unclassified.  
1 (bases 1 to 2648)  
Ford, J., Ho, A.S.Y. and Pace, A.  
Interleukin-1 receptor antagonist and uses thereof  
Patent: US 6541623-A 6 01-APR-2003;  
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## RESULT 14

AX069309  
LOCUS AX069309 2648 bp DNA linear PAT 25-JAN-2001  
DEFINITION Sequence 6 from Patent WO0102571.

ACCESSION AX069309

VERSION AX069309.1 GI:12579181

## KEYWORDS

SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 Ford, J. and Pace, A.

A interleukin-1 receptor antagonist and uses thereof

TITLE Patent: WO 0102571-A 6 11-JAN-2001;

JOURNAL HYSEQ, INC. (US)

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Db	2192	TAAATGATCCCTGCTCTGTTTACATTTCTGTTGTTCCCTCCACAAATGTACC	2251
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Db 2371 CCAATCTATCTTGGCTCACTCGCTCTGGGGGAAAGCTAGCTGCGCATGCTATGACAGCGCT 2430

QY 2399 ATAAAGAGACTTACGTTGGTAAATAAAGTCTCTGCGCACCGACACATTAAGTGAACCT 2458

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QY 2459 AGAAGCAGAGACTCTCTGAGATAATCCATGTTTGTGTTT-AAAGTTGCTAGTGTGTTGTT 2517

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QY 2518 CTAACCTGTTATGCAGCAATAGATAAATAATATGCAGAGAAAGAGA 2563

Db 2551 CTAACCTGTTATGCAGCAATAGATAAATAATATGCAGAGAAAGAGA 2596

RESULT 15

AF186094

LOCUS

DEFINITION Homo sapiens interleukin-1 receptor antagonist homolog (IL1HV1)

ACCESSION AF186094

VERSION AF186094.1 GI:6049804

KEYWORDS

SOURCE

ORGANISM Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2720)

AUTHORS Mulero,J.J., Pace,A.M., Nelken,S.T., Loeb,D.B., Correa,T.R., Drmanac,R. and Ford,J.E.

TITLE IL1HV1: A novel interleukin-1 receptor antagonist gene

JOURNAL Biochem. Biophys. Res. Commun. 263 (3), 702-706 (1999)

MEDLINE 99443727

PUBMED 10512743

REFERENCE 2 (bases 1 to 2720)

AUTHORS Mulero,J.J., Pace,A.M., Nelken,S.T., Loeb,D.B., Correa,T.R., Drmanac,R. and Ford,J.E.

TITLE Direct Submission

JOURNAL Submitted (13-SEP-1999) Functional Genomics, HYSEQ Inc., 670

Almanor Ave., Sunnyvale, CA 94086, USA

FEATURES

Location/Qualifiers

1..2720

/organism="Homo sapiens"

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1..2720

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/note="IL-1ra homolog"

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ORIGIN

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Best Local Similarity 99.4%; Pred. No. 0;

Matches 2550; Conservative 0; Mismatches 11; Indels 5; Gaps 5;

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Db 194 TGAAGAGCTCGCAATTGAAGTGTCTTTATCTGCATAATAACACAGCTTCTAGCTGGAGGC 253

QY 121 TGCATCGAGGGAAGGTCAATTAAGGTGAAGAGATCAGCGTGTGCCCAATCGTGGCTGG 180

Db 254 TGCATCGAGGGAAGGTCAATTAAGGTGAAGAGATCAGCGTGTGCCCAATCGTGGCTGG 313

QY 181 ATGCCAGAGCTGTCCCGCTCATCTCTGGGTGTCCAGGTGGGAAGCCAGTGCCTGTCTATG 240

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QY 241 GGGTGGGCGAGAGCGGACTCTAACAACATAGAGCCAGTGAACATCATGAGCTCTATCTTG 300

Db 374 GGGTGGGCGAGAGCGGACTCTAACAACATAGAGCCAGTGAACATCATGAGCTCTATCTTG 433

QY 301 GTGCCAAGAAATCCAAAGAGCTTCACTTCTACCGGGGGAACATGGGGTCACTCCAGCT 360

Db 434 GTGCCAAGAAATCCAAAGAGCTTCACTTCTACCGGGGGAACATGGGGTCACTCCAGCT 493

QY 361 TCGAGTCCGGCTGCTACCGGGCTGGTTCCTGTGCACGGTGCCTGAAGCCGATCAGCCG 420

Db 494 TCGAGTCCGGCTGCTACCGGGCTGGTTCCTGTGCACGGTGCCTGAAGCCGATCAGCCG 553

QY 421 TCAGACTCACCCAGCTTCCGAGAAATGGTGGTGGAAATGCCCCCATCAGAGCTTCTACT 480

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QY 541 GTGAGGGTGTGAGTGGAGAGACCCATGGGGCAATCACTCTTCTGTCTCAGGACCCC 600

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Db 733 CAGGCTGACTAGTGGGCACCTGACCACTTGTCTTCTGTGTTCCAGTTCATATAAAT 792

QY 661 CTGAGATTGGAGCTCAGTCCAGGGTCTTCCGCCATCTGATGGTGTCTGTCTGGAAAC 720

Db 793 CTGAGATTGGAGCTCAGTCCAGGGTCTTCCGCCATCTGATGGTGTCTGTCTGGAAAC 852

QY 721 CTGTGAAAACCATGTGGGTAAATGGGAATAACATGAAAGATTTCTGTGGGGTGGG 780

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QY 781 GTGGGGGAGTGTGGGAATCATTCCTGCTTAATGGTAACTGACAAAGTGTACCTTGAGCC 840

Db 913 GTGGGGGAGTGTGGGAATCATTCCTGCTTAATGGTAACTGACAAAGTGTACCTTGAGCC 972

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QY 961 TGGCCCGAGCCCGCCCTTCCCTTT-ATCTGCGCACTGTCTATATGCTACCTTTTCTATC 1019

Db 1093 TGGCCCGAGCCCGCCCTTCCCTTTAATCTTCCCACTGTCTATATGCTACCTTTCTATC 1152

QY 1020 TCTTCCCTCATCATCTTGTGTGGGCATGAGAGGTGGTGTGTCAGAGAAATGGTTGG 1079

Db 1153 TCTTCCCTCATCATCTTGTGTGGGCATGAGAGGTGGTGTGTCAGAGAAATGGCTCG 1212

QY 1080 AGCTCAGAGATAAAGATAGTGGGTATGCTGATCTCTCTTTTAAACCCCAAGATACA 1139

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QY	2159	TAAATGATCCCTGCTCTCTGTTTACATTTCTGTTGTTGTTCCCTCCCAATGTACC	2218
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Search completed: March 13, 2005, 15:49:10  
Job time : 11345.9 secs

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VERSION	AX080404.1	GI:13159847			
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SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				



Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 Nicklin,M. and Barton,J.  
The il-11 gene and polypeptide products  
Patent: WO 0105974-A 16 25-JAN-2001;  
Interleukin Genetics, Inc. (US)

## FEATURES

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1. .73  
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## ORIGIN

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## Db

## RESULT 3

## HSA242738

## LOCUS

DEFINITION Homo sapiens mRNA for interleukin-1-like protein 1 (IL1L1 gene)  
transcript 2.

## ACCESSION

AJ242738

## VERSION

IL1L1 gene; interleukin-1-like protein 1.

## KEYWORDS

Homo sapiens (human)

## SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 Barton,J.L., Herbet,R., Bosio,D., Higgins,L. and Nicklin,M.J.  
A tissue specific IL-1 receptor antagonist homolog from the IL-1  
cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities  
Eur. J. Immunol. 30 (11), 3299-3308 (2000)

## JOURNAL

MEDLINE

PUBMED

11093146

## REFERENCE

2 (bases 1 to 2604)

Nicklin,M.J.

## TITLE

Direct Submission  
Submitted (09-JUN-1999) Nicklin M.J., Division of Molecular and  
Genetic Medicine, University of Sheffield, Royal Hallamshire  
Hospital, Glossop Road, Sheffield, S10 2UF, UNITED KINGDOM

## JOURNAL

Location/Qualifiers

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polya\_site

ORIGIN

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## Db

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## RESULT 4

## BC024747

## LOCUS

DEFINITION Homo sapiens interleukin 1 family, member 5 (delta), transcript  
variant 2, mRNA (cdna clone MGC:29840 IMAGE:4996939), complete cds.

## ACCESSION

BC024747

## VERSION

BC024747.1

GI:19353229

MGC.

ORGANISM

Homo sapiens (human)

Homo sapiens

Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

AUTHORS

1 (bases 1 to 2692)

Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,

Altshul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

Hopkins,R.P., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,

Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,

Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,

Scheetz,T.E., Brownstein,M.J., Uscin,T.B., Toshiyuki,S.,

Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,

Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,

McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,

Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,

Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,

Fahney,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S.,

Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,

Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,

Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,

Butterfield,V.S., Krzywinski,M.I., Skalska,U., Smalhus,D.E.,

Schmerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 2692)

Strausberg,R.

Direct Submission

Submitted (01-MAR-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome

Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseg, H.,

Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,

A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 42 Row: k Column: 16

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 27894309.

Location/Qualifiers

FEATURES

[illegible]

	source	1. .2692 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MGC:29840 IMAGE:4996939" /tissue_type="Placenta, choriocarcinoma" /clone_lib="NIH_MGC_10" /lab_host="DH10B" /notes=Vector: pCMV-SPORT6"
	gene	1. .2692 /genes="IL1P5" /note="synonyms: FIL1(Delta), FIL1D, IL1RP3, IL1HYL, FIL1, IL1L1, MGC29840" /db_xref="LocusID:26525" /db_xref="MIM:605507" 134. .601 /genes="IL1P5" /codon_start=1 /product="interleukin 1 family, member 5" /protein_id="AAH24747.1" /db_xref="GI:19353230" /db_xref="LocusID:26525" /db_xref="MIM:605507" /translation="MWLSGALCFRMDKSAIKLVLYLNQLLAGGLHAGKVIGKEETISV VNRMLDASLPVLGVGGSCQLSCGVGPPTLTLEPVNIMELYLGAKESKSFYFR RDMLGTSPESAAYPGWFLCTVPADQPVRLTQLPENGGWNAPITDFYQQCD"
	CDS	Query Match 100.0%; Score 42; DB 9; Length 2692; Best Local Similarity 100.0%; Pred. No. 0.0013; Mismatches 0; Indels 0; Gaps 0; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	ORIGIN	Gy 1 AAGGAAGGAGGAGAAGGAGGAGGAGTGTAAGGAAGGAGTGAAA 42       Db 62 AAGGAAGGAGGAGAAGGAGGAGGAGTGTAAGGAAGGAGTGAAA 103 
	RESULT 5	
	AX080431	LOCUS AX080431 6540 bp DNA linear PAT 22-FEB-2001
	DEFINITION	Sequence 43 from Patent WO0105974.
	ACCESSION	AX080431
	VERSION	AX080431.1 GI:13159871
	KEYWORDS	.
	SOURCE	Homo sapiens (human)
	ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
	REFERENCE	1 Nicklin,M. and Barton,J. The il-1l1 gene and polypeptide products Patent: WO 0105974-A 43 25-JAN-2001; Interleukin Genetics, Inc. (US) Location/Qualifiers
	AUTHORS	1. .6540 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
	TITLE	
	JOURNAL	
	FEATURES	source Query Match 100.0%; Score 42; DB 6; Length 6540; Best Local Similarity 100.0%; Pred. No. 0.0012; Mismatches 0; Indels 0; Gaps 0; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	ORIGIN	Gy 1 AAGGAAGGAGGAGAAGGAGGAGGAGTGTAAGGAAGGAGTGAAA 42       Db 480 AAGGAAGGAGGAGAAGGAGGAGGAGTGTAAGGAAGGAGTGAAA 521 
	RESULT 6	
	HSJ271338	LOCUS HSJ271338 6540 bp DNA linear PRI 18-APR-2002
	DEFINITION	Homo sapiens IL1L1 gene for interleukin-1 like protein 1, exons
	ACCESSION	HSJ271338
	VERSION	HSJ271338.1 GI:6729586
	KEYWORDS	IL1L1 gene; interleukin-1 like protein 1. Homo sapiens (human)
	SOURCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
	ORGANISM	1 Barton,J.L., Herbet,R., Bosio,D., Higgins,L. and Nicklin,M.J. A tissue specific IL-1 receptor antagonist homolog from the IL-1 cluster lacks IL-1, IL-lra, IL-18 and IL-18 antagonist activities Eur. J. Immunol. 30 (11), 3299-3308 (2000)
	REFERENCE	1 Barton,J.L., Herbet,R., Bosio,D., Higgins,L. and Nicklin,M.J. A tissue specific IL-1 receptor antagonist homolog from the IL-1 cluster lacks IL-1, IL-lra, IL-18 and IL-18 antagonist activities Eur. J. Immunol. 30 (11), 3299-3308 (2000)
	AUTHORS	1 Barton,J.L., Herbet,R., Bosio,D., Higgins,L. and Nicklin,M.J. A tissue specific IL-1 receptor antagonist homolog from the IL-1 cluster lacks IL-1, IL-lra, IL-18 and IL-18 antagonist activities Eur. J. Immunol. 30 (11), 3299-3308 (2000)
	TITLE	Direct Submission
	JOURNAL	Submitted (17-JAN-2000) Nicklin M.J.H., Division of Molecular and Genetic Medicine, University of Sheffield, Royal Hallamshire Hospital, Sheffield, South Yorkshire, UNITED KINGDOM
	MEDLINE	20545212 11093146
	PUBMED	11093146
	REFERENCE	2 (bases 1 to 6540) Nicklin,M.J.H.
	AUTHORS	1 Barton,J.L., Herbet,R., Bosio,D., Higgins,L. and Nicklin,M.J. A tissue specific IL-1 receptor antagonist homolog from the IL-1 cluster lacks IL-1, IL-lra, IL-18 and IL-18 antagonist activities Eur. J. Immunol. 30 (11), 3299-3308 (2000)
	TITLE	Direct Submission
	JOURNAL	Submitted (17-JAN-2000) Nicklin M.J.H., Division of Molecular and Genetic Medicine, University of Sheffield, Royal Hallamshire Hospital, Sheffield, South Yorkshire, UNITED KINGDOM
	FEATURES	source 1. .6540 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="2" /map="2q13" /clone="PAC 131J6" 451. .6522 /gene="IL1L1" Join(<451..524,1193..1248,2631..2716,3905..4032, 4234..6522) /gene="IL1L1" 451..524 /gene="IL1L1" /number=1 457. .507 /gene="IL1L1" /note="unnamed protein product; uORF" /codon_start=1 /protein_id="CAB67703.1" /db_xref="GI:6729587" /db_xref="UniProt/TREMBL:Q9NY32" /translation="MAGRKDRGRKEGEKGE" 525. .968 /gene="IL1L1" /number=1 Join(<969..1022,1193..1248,2631..2716,3905..4032, 4234..6522) /gene="IL1L1" /note="alternative" 969..1022 /gene="IL1L1" /number=2 1023..1192 /gene="IL1L1" /number=2 1193..1248 /gene="IL1L1" /number=3 Join(1220..1248,2631..2716,3905..4032,4234..4458) /gene="IL1L1" /function="putative cytokine or cytokine antagonist" /codon_start=1 /product="interleukin-1 like protein 1" /protein_id="CAB67704.1" /db_xref="GI:6729588" /db_xref="GOA:Q9UBH0" /db_xref="UniProt/Swiss-Protein:Q9UBH0" /translation="MWLSGALCFRMDKSAIKLVLYLNQLLAGGLHAGKVIGKEETISV VNRMLDASLPVLGVGGSCQLSCGVGPPTLTLEPVNIMELYLGAKESKSFYFR RDMLGTSPESAAYPGWFLCTVPADQPVRLTQLPENGGWNAPITDFYQQCD"

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Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAGGAGGGAGAGAGGGAAGGAGTGAAGGAGGAGTGAAG 42
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Db 1339 AAGGAGGAGGGAGAGAGGGAAGGAGTGAAGGAGGAGTGAAG 1380
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RESULT 12
LOCUS AX069311 7605 bp DNA linear PAT 25-JAN-2001
DEFINITION Sequence 8 from Patent WO0102571.
ACCESSION AX069311
VERSION AX069311.1 GI:12579183
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ford, J. and Pace, A.
TITLE A interleukin-1 receptor antagonist and uses thereof
JOURNAL Patent: WO 0102571-A 8 11-JAN-2001;
HYSEQ, INC. (US)
FEATURES
    source          Location/Qualifiers
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

ORIGIN

Query Match      100.0%; Score 42; DB 6; Length 7605;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAGGAGGGAGAGAGGGAAGGAGTGAAGGAGGAGTGAAG 42
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Db 1339 AAGGAGGAGGGAGAGAGGGAAGGAGTGAAGGAGGAGTGAAG 1380
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RESULT 13
LOCUS AC016724 197308 bp DNA linear PRI 09-JAN-2002
DEFINITION Homo sapiens BAC clone RP11-339F22 from 2, complete sequence.
ACCESSION AC016724
VERSION AC016724.11 GI:14718389
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Sulston, J.E. and Waterston, R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074
REFERENCE 2
AUTHORS Armstrong, J. and Haakenson, W.
TITLE The sequence of Homo sapiens BAC clone RP11-339F22
JOURNAL Unpublished (2001)
REFERENCE 3
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (04-DEC-1999) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE 4
AUTHORS Waterston, R.H.
TITLE

```

TITLE Direct Submission  
JOURNAL Submitted (14-JUL-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 5 (bases 1 to 197308)  
AUTHORS Waterston, R.  
TITLE Direct Submission  
JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
COMMENT On Jul 14, 2001 this sequence version replaced gi:13431151.  
----- Genome Center  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: http://genome.wustl.edu/gsc  
Contact: sapiens@wustl.edu  
----- Summary Statistics  
-----  
Center project name: H\_NH0339F22  
-----

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:  
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:  
The RPC1-11 human BAC library was made from the blood of one male donor, as described by Ooegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)

VECTOR: pBACe3.6  
NEIGHBORING SEQUENCE INFORMATION:  
The clone sequenced to the left is RP11-725J3; the clone sequenced to the right is RP11-97J14. Actual start of this clone is at base position 1 of RP11-339F22; actual end is at base position 197308 of RP11-339F22.

Data from AC084280 and AC024704 was used to finish this clone, AC016724. Polymorphisms have been identified between AC024704 and AC016724.

Sequence derived from pcr from base position 148683 to 149264.

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JOURNAL Submitted (03-APR-2003) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 6 (bases 1 to 162771)

AUTHORS Wilson.R.

TITLE Direct Submission

JOURNAL Submitted (30-MAY-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

COMMENT On Apr 3, 2003 this sequence version replaced gi:27923720.

----- Genome Center -----  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: <http://genome.wustl.edu/gsc>  
Contact: [sapiens@wustl.edu](mailto:sapiens@wustl.edu)  
----- Summary Statistics -----  
Center project name: H\_NHO366H04  
-----

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:  
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:  
The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:  
This sequence is not the entire insert of the clone. This clone is overlapped by AC108073.

Data from AC13529 was used to finish this clone.

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repeat_region	2906..3219
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University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 On Jan 29, 2003 this sequence version replaced gi:26006685.  
 ----- Genome Center  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: <http://genome.wustl.edu/gsc>  
 Contact: [sapiens@wustl.wustl.edu](mailto:sapiens@wustl.wustl.edu)  
 ----- Summary Statistics  
 Center project name: H\_NH0458M01  
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## COMMENT

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:  
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

## MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

## SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatenno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>  
 VECTOR: pBACe3.6

## NEIGHBORING SEQUENCE INFORMATION:

This sequence is the entire insert of the clone.

## FEATURES

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 13, 2005, 11:56:15 ; Search time 127.576 Seconds  
(without alignments)  
11636.250 Million cell updates/sec

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Perfect score: 39  
Sequence: 1 ttgaggaaacagcagactccacagctccgcagagaa 39

Scoring table: IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST.\*

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2: gb\_est2.\*  
3: gb\_hic.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_gss1.\*  
9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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3	25	64.1	444	6	CB745486	CB745486 AMGNNUC-M
4	24.8	63.6	264	8	AZ401556	AZ401556 IMOL168P17
5	24.8	63.6	854	7	CO805958	CO805958 AGENCOURT
6	24	61.5	805	5	BU354596	BU354596 603473139
7	23.8	61.0	381	2	BE93964	BE93964 UI-M-BZ1-
8	23.8	61.0	633	7	CK831100	CK831100 405458 B
9	23.6	60.5	523	1	AV604210	AV604210 AV604210
10	23.6	60.5	1046	5	BX373721	BX373721 BX373721
11	23.2	59.5	656	9	CE232012	CE232012 tigr-gss-
12	23.2	59.5	766	5	BP700567	BP700567 BP700567
13	23.2	59.5	794	5	BU708233	BU708233 UI-M-FCO-
14	23	59.0	443	8	BZ206975	BZ206975 CH230-425
15	22.8	58.5	490	1	AI762761	AI762761 wh83e11.x
16	22.8	58.5	507	1	AU200748	AU200748 AU200748
17	22.8	58.5	563	4	BJ116536	BJ116536 BJI16536
18	22.8	58.5	629	1	AU200217	AU200217 AU200217
19	22.8	58.5	752	5	BU363211	BU363211 603585713
20	22.6	57.9	365	6	CA360753	CA360753 634412 NC
21	22.6	57.9	702	4	BG484677	BG484677 602505856
22	22.6	57.9	1155	8	CC255590	CC255590 CH261-124
23	22.4	57.4	415	2	BF773640	BF773640 283016 MA
24	22.4	57.4	645	9	CE176613	CE176613 tigr-gss-

C	25	22.2	56.9	198	1	AU255348	AU255348
C	26	22.2	56.9	237	6	BY596552	BY596552 BX596552
C	27	22.2	56.9	247	7	W83796	W83796 mf33c03.r1
C	28	22.2	56.9	255	1	AA184891	AA184891 mu48a08.r
C	29	22.2	56.9	257	5	BQ176985	BQ176985 UI-M-DJ2-
C	30	22.2	56.9	274	1	AA015339	AA015339 mh13b08.r
C	31	22.2	56.9	300	7	CR519216	CR519216 CR519216
C	32	22.2	56.9	336	4	BG090476	BG090476 mac07b03.
C	33	22.2	56.9	356	5	BY467369	BY467369 BY467369
C	34	22.2	56.9	360	4	BG090598	BG090598 mac08f06.
C	35	22.2	56.9	363	2	BB766156	BB766156 BB766156
C	36	22.2	56.9	370	4	BG092249	BG092249 mac07b03.
C	37	22.2	56.9	385	5	BU756272	BU756272 UI-1-CFO-
C	38	22.2	56.9	386	2	BF100852	BF100852 601753788
C	39	22.2	56.9	388	2	BE849929	BE849929 uw09f08.y
C	40	22.2	56.9	391	6	BY527295	BY527295 BY527295
C	41	22.2	56.9	401	2	BE989206	BE989206 UI-M-BZ1-
C	42	22.2	56.9	416	4	BM668586	BM668586 UI-E-CK1-
C	43	22.2	56.9	418	1	AI414767	AI414767 ms59h02.x
C	44	22.2	56.9	442	1	AA267559	AA267559 val6908.r
C	45	22.2	56.9	448	2	BE989363	BE989363 UI-M-BZ1-

## ALIGNMENTS

RESULT 1  
BX477358  
LOCUS BX477358 338 bp mRNA linear EST 04-SEP-2003  
DEFINITION DKFZp686022193\_r1.686 (synonym: hlcc3) Homo sapiens CDNA clone  
ACCESSION DKFZp686022193.5, mRNA sequence.  
VERSION BX477358  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 338)  
AUTHORS Ansoerg,W., Krieger,S., Regiert,T., Rittmueller,C., Schwager,B.,  
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and  
Wiemann,S.  
TITLE EST (Ansoerg,W., Krieger,S., Regiert,T., Rittmueller,C., et al.)  
JOURNAL Unpublished (2003)  
COMMENT Contact: MIPS  
MIPS  
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
Heidelberg/Germany) within the CDNA sequencing consortium of the  
German Genome Project.  
No sl sequence available.  
This clone (DKFZp686022193) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES  
source  
1..338  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZp686022193"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="686 (synonym: hlcc3)"  
/notes="Vector: pTriplex2; Site\_1: SfiIA; Site\_2: SfiIB;  
CDNA-collection"

## ORIGIN

Query Match 66.7%; Score 26; DB 5; Length 338;  
Best Local Similarity 100.0%; Pred. No. 67;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 14 AGACTCCACAGCTCCGCCAGGAGAA 39
|||||
Db 1 AGACTCCACAGCTCCGCCAGGAGAA 26

RESULT 2
AW141829 424 bp mRNA linear EST 30-OCT-1999
LOCUS EST291936 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone
DEFINITION RGIC187 5' end similar to guanine nucleotide-binding protein Rat,
mRNA sequence.
ACCESSION AW141829
VERSION AW141829.1 GI:6161680
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 424)
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
TITLE Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
For clone availability, additional sequence and expression
information related to this EST please check the TIGR Rat Gene
Index (http://www.tigr.org/cdb/rgr/rgr.html). To order a clone
contact the ATCC (http://www.atcc.org/atcc.html).
Seq primer: M13 Reverse.
Location/Qualifiers
1..424
/organism="Rattus sp."
/mol_type="mRNA"
/db_xref="taxon:10118"
/clone="RGIC187"
/dev_stage="embryo 8, 12, 18 dpc"
/clone_lib="Normalized rat embryo, Bento Soares"
/note="Vector: pT73Pac; Site_1: EcoRI; Site_2: NotI"

FEATURES
source
QY 6 GAACAGCAGACTCCACAGCTCCGCCAGGAGA 38
|||||
Db 343 GAACAGCGGAGACCCACAGCTCCGCTAGGAGA 311

RESULT 3
CB745486/c 444 bp mRNA linear EST 11-APR-2003
LOCUS AMGNNUC:MRBE3-00043-A6-A rat brain E15 (10374) Rattus norvegicus
DEFINITION cDNA clone mrbe3-00043-a6 5', mRNA sequence.
ACCESSION CB745486
VERSION CB745486.1 GI:29812788
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 444)
AUTHORS Angen EST Program.
TITLE Angen Rat EST Program

JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 0043 row: a column: 6.
Location/Qualifiers
1..444
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="mrbe3-00043-a6"
/tissue_type="brain E15"
/clone_lib="rat brain E15 (10374)"
/note="Vector: pBCB; Site_1: BstXI; Site_2: NotI; rat
brain E15"

FEATURES
source
QY 6 GAACAGCAGACTCCACAGCTCCGCCAGGAGA 38
|||||
Db 366 GAACAGCGGAGACCCACAGCTCCGCTAGGAGA 334

RESULT 4
AZ401556 264 bp DNA linear GSS 03-OCT-2000
LOCUS IM0168P17F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
DEFINITION clone UUGCIM0168P17 F, genomic survey sequence.
ACCESSION AZ401556
VERSION AZ401556.1 GI:10516630
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 264)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0168 row: P column: 17
Seq primer: CGTTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 264.
Location/Qualifiers
1..264
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0168P17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

```





**TITLE** Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000

**JOURNAL** Bovine ESTs

**MEDLINE** Nucleic Acids Res. 29 (22), E108 (2001)

**PUBMED** 21570554

**COMMENT** 11713328

Contact: Yoshikazu Sugimoto  
Animal Genetics Division  
Shirakawa Institute of Animal Genetics  
Odakura, Nishigo, Nishi-Shirakawa, Fukushima 961-8061, Japan

Tel: 81-248-25-5641

Fax: 81-248-25-5725

Email: kazusugi@cococ.ocn.ne.jp

Single pass sequencing.  
This clone was obtained from a polyA-deleted cDNA library.

#### FEATURES

source

1. .523

/organism="Bos taurus"

/mol\_type="mRNA"

/db\_xref="taxon:9913"

/clone="EIK1021D06"

/tissue\_type="kidney"

/dev\_stage="fetus"

/lab\_host="DH10B"

/clone\_lib="Bos taurus kidney fetus"

/note="Vector: pZLI; Site\_1: SalI; Site\_2: NotI; Poly A was deleted from a NotI site"

#### ORIGIN

**Query Match** 60.5%; Score 23.6; DB 1; Length 523;  
**Best Local Similarity** 76.3%; Pred. No. 5.2e+02;  
**Matches** 29; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

**QY** 2 TGAGGAACAGGACACTCCACAGCTCCCGCCAGAGAA 39

**Db** 466 TCAGGATCGACAGACTCCAGTCTCCAGCCAGCACA 503

#### RESULT 10

**LOCUS** BX373721

**DEFINITION** BX373721 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0D1071YH11 3-PRIME, mRNA sequence.

**ACCESSION** BX373721

**VERSION** BX373721.1

**KEYWORDS** EST.

**SOURCE** Homo sapiens (human)

**ORGANISM** Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

**REFERENCE** 1 (bases 1 to 1046)

**AUTHORS** Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

**TITLE** Full-length cDNA libraries and normalization

**JOURNAL** Unpublished (2001)

**COMMENT** Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1718.f

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CS0BAK063CB10NM1&c=1718.f.

#### FEATURES

source

1. .1046

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0D1071YH11"

/tissue\_type="PLACENTA COT 25-NORMALIZED"

#### ORIGIN

**Query Match** 60.5%; Score 23.6; DB 5; Length 1046;  
**Best Local Similarity** 76.3%; Pred. No. 5.3e+02;  
**Matches** 29; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

**QY** 2 TGAGGAACAGGACACTCCACAGCTCCCGCCAGAGAA 39

**Db** 576 TCAGGACAGGACACTCACTGCTCTCCAGTAGAA 613

#### RESULT 11

**LOCUS** CE232012

**DEFINITION** tigr-gss-dog-1700033348863 Dog Library Canis familiaris genomic, genomic survey sequence.

**ACCESSION** CE232012

**VERSION** CE232012.1

**KEYWORDS** GSS.

**SOURCE** Canis familiaris (dog)

**ORGANISM** Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

**REFERENCE** 1 (bases 1 to 656)

**AUTHORS** Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,

Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and

Venter, J.C.

**TITLE** The dog genome: survey sequencing and comparative analysis

**JOURNAL** Science 301 (5641), 1898-1903 (2003)

**MEDLINE** 22875432

**PUBMED** 14512627

**COMMENT** Contact: Kirkness EF

The Institute for Genomic Research

Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,

Rockville, MD 20850, USA

Tel: 301-838-0200

Fax: 301-838-0208

Email: ekirknes@tigr.org

Class: shotgun.

#### FEATURES

source

1. .656

/organism="Canis familiaris"

/mol\_type="genomic DNA"

/strain="Standard Poodle"

/db\_xref="taxon:9615"

/clone\_lib="Dog Library"

/note="Site 1: BstXI; Libraries were prepared from peripheral blood"

#### ORIGIN

**Query Match** 59.5%; Score 23.2; DB 9; Length 656;  
**Best Local Similarity** 77.8%; Pred. No. 7.3e+02;  
**Matches** 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

**QY** 4 AGAACAGGACACTCCACAGCTCCCGCCAGAGAA 39

**Db** 503 AGAACATCGAGTAGCAGATCCAGCCAGGTGAA 538

#### RESULT 12

**LOCUS** BP700567

**DEFINITION** BP700567 Osada Taira anterior neuroectoderm (ANE) PCS105 cDNA library Xenopus laevis cDNA clone XL490c06ex 5', mRNA sequence.

**ACCESSION** BP700567

**VERSION** BP700567.1

**KEYWORDS** EST.

**SOURCE** Xenopus laevis (African clawed frog)





/clone="CH230-42508"

/sex="Female"

/cell\_type="Brain"

/clone\_lib="CHORI-230 Segment 2"

/notes="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;

CHORI-230 Rat (BN/SmHsd/MCW) BAC library produced by

Pieter de Jong"

## ORIGIN

Query Match 59.0%; Score 23; DB 8; Length 443;

Best Local Similarity 74.4%; Pred. No. 8.4e+02;

Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 TTGAGGAACAGCGAGACTCCACAGCTCCGCCAGGAGAA 39

| | | | | | | | | | | | | | | | | | | | | |

Db 22 TAGAGGACAGCGAGAAACCCAAAGCCCGAGTCAGGGAA 60

## RESULT 15

AI762761/c

LOCUS

DEFINITION wh83e11.x1 NCI\_CGAP\_C111 Homo sapiens CDNA clone IMAGE:2387372 3',

mRNA sequence.

AI762761

AI762761.1 GI:5178428

EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 490)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: [cgaps@mail.nih.gov](mailto:cgaps@mail.nih.gov)

Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,

M.D., Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Sequencing by: Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Insert Length: 1107 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 477.

Location/Qualifiers

## FEATURES

source

1..490

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2387372"

/tissue\_type="B-cell, chronic lymphocytic leukemia"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP C111"

/notes="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand CDNA

was primed with a Not I - oligo(dT) primer [5,

T 3']; double-stranded CDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of the modified pT73 vector.

Library is normalized, and was constructed by Bento

Soares and M.Fatima Bonaldo."

## ORIGIN

Query Match 58.5%; Score 22.8; DB 1; Length 490;

Best Local Similarity 79.4%; Pred. No. 1e+03;

Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 GAGGAACAGCGAGACTCCACAGCTCCCGCAGGA 36

Db 278 GAGCAACAGGGAAATTCACAGCTGCTCCAGAA 245

Search completed: March 13, 2005, 18:13:56

Job time : 142.576 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 13, 2005, 11:14:57 ; Search time 172.432 Seconds  
(without alignments)  
10959.418 Million cell updates/sec

Title: US-09-617-720A-2  
Perfect score: 39  
Sequence: 1 ttgaggaaacaggcagactccacagctccgccaggagaa 39

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

#### Database :

GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sta.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	100.0	39	6	AX080390 Sequence
2	39	100.0	2613	9	AJ242737 Homo sapi
3	37.4	95.9	54	6	AX080406 Sequence
4	37.4	95.9	2701	6	CQ722801 Sequence
5	37.4	95.9	2720	9	AF186094 Homo sapi
6	37.4	95.9	5751	6	BD211436 A novel i
7	37.4	95.9	5751	6	AR181996 Sequence
8	37.4	95.9	5751	6	AR221130 Sequence
9	37.4	95.9	5751	6	AR302958 Sequence
10	37.4	95.9	5751	6	AX069310 Sequence
11	37.4	95.9	6540	6	AX080431 Sequence
12	37.4	95.9	6540	9	HS242737 Homo sapi
13	37.4	95.9	7604	9	AF216693 Homo sapi
14	37.4	95.9	7605	6	BD211437 A novel i
15	37.4	95.9	7605	6	AR181997 Sequence
16	37.4	95.9	7605	6	AR221131 Sequence
17	37.4	95.9	7605	6	AR302959 Sequence
18	37.4	95.9	7605	6	AX069311 Sequence
19	37.4	95.9	197308	9	AC016724 Homo sapi

C 20	29.4	75.4	197308	9	AC016724	Homo sapi
C 21	25.4	65.1	90147	2	AC135832	Rattus no
C 22	25	64.1	247903	2	AC127185	Rattus no
C 23	24.8	63.6	7733	10	AF233337	Mus muscu
C 24	24.8	63.6	91841	10	AL606971	Mouse DNA
C 25	24.4	62.6	125495	9	AL359914	Human DNA
C 26	23.8	61.0	154708	2	AC024443	Homo sapi
C 27	23.8	61.0	170979	9	AC007950	Homo sapi
C 28	23.8	61.0	171456	9	AC023591	Homo sapi
C 29	23.8	61.0	177432	9	AC118274	Homo sapi
C 30	23.8	61.0	203912	9	AC008755	Homo sapi
C 31	23.8	61.0	230882	9	AC131689	Mus muscu
C 32	23.2	59.5	3868	5	BC073106	Xenopus l
C 33	23.2	59.5	149556	9	AC146478	Pan trogl
C 34	23.2	59.5	198155	2	BS000632	Human DNA
C 35	23	59.0	101196	9	HS463A9	Human DNA
C 36	23	59.0	214497	2	AC102558	Mus muscu
C 37	23	59.0	279315	2	AC132765	Rattus no
C 38	23	59.0	342581	2	AC132742	Rattus no
C 39	22.8	58.5	3071	6	CQ609104	Sequence
C 40	22.8	58.5	31261	3	U41278	Caenorhabdi
C 41	22.8	58.5	45258	2	AC015395	Drosophil
C 42	22.8	58.5	144090	2	AC150031	Dasyopus n
C 43	22.8	58.5	175223	9	AC004617	Homo sapi
C 44	22.8	58.5	186218	3	AC023680	Drosophil
C 45	22.8	58.5	245482	2	AC110679	Rattus no

#### ALIGNMENTS

RESULT 1  
AX080390  
LOCUS AX080390 39 bp DNA linear PAT 22-FEB-2001  
DEFINITION Sequence 2 from Patent WO0105974.  
ACCESSION AX080390  
VERSION AX080390.1 GI:13159841  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Nicklin,M. and Barton,J.  
TITLE The il-11 gene and polypeptide products  
JOURNAL Patent: WO 0105974-A 2 25-JAN-2001;  
Interleukin Genetics, Inc. (US)  
FEATURES  
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LOCUS HSA242737  
DEFINITION Homo sapiens mRNA for interleukin-1-like protein-1 (IL1L1 gene), transcript 1.  
ACCESSION AJ242737  
VERSION AJ242737.1 GI:6165333  
KEYWORDS IL1L1 gene; interleukin-1-like protein-1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens



Db 813 TGGAGGAACAGGCAGAGACTCCACAGCTCCCGCCAGGAGAA 851

RESULT 7  
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 LOCUS AR181996 5751 bp DNA linear PAT 20-APR-2002  
 DEFINITION Sequence 7 from patent US 6337072.  
 ACCESSION AR181996  
 VERSION AR181996.1 GI:20224912  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 5751)  
 AUTHORS Ford,J. and Pace,A.  
 TITLE Interleukin-1 receptor antagonist and recombinant production thereof  
 JOURNAL Patent: US 6337072-A 7 08-JAN-2002;  
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RESULT 8  
 AR221130  
 LOCUS AR221130 5751 bp DNA linear PAT 26-SEP-2002  
 DEFINITION Sequence 7 from patent US 6426191.  
 ACCESSION AR221130  
 VERSION AR221130.1 GI:23328015  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 5751)  
 AUTHORS Ford,J. and Pace,A.  
 TITLE Assays involving an IL-1 receptor antagonist  
 JOURNAL Patent: US 6426191-A 7 30-JUL-2002;  
 FEATURES Location/Qualifiers  
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 LOCUS AR302958 5751 bp DNA linear PAT 12-JUN-2003  
 DEFINITION Sequence 7 from patent US 6541623.  
 ACCESSION AR302958  
 VERSION AR302958.1 GI:31691558  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 5751)

AUTHORS Ford, J., Ho, A.S.Y. and Pace, A.  
TITLE Interleukin-1 receptor antagonist and uses thereof  
JOURNAL Patent: US 6541623-A 7 01-APR-2003,  
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LOCUS Sequence 7 from Patent WO0102571.

ACCESSION AX069310

VERSION AX069310.1 GI:12579182

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 Ford, J. and Pace, A.

A interleukin-1 receptor antagonist and uses thereof

Patent: WO 0102571-A 7 11-JAN-2001;

HYSEQ, INC. (US)

FEATURES

Location/Qualifiers

source 1..5751

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Db 813 TGGAGGAACAGGCAGACTCCACAGCTCCCGCCAGGAGAA 851

## RESULT 11

AX080431 6540 bp DNA linear PAT 22-FEB-2001

LOCUS Sequence 43 from Patent WO0105974.

DEFINITION

ACCESSION AX080431

VERSION AX080431.1 GI:13159871

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 Nicklin, M. and Barton, J.

The il-11 gene and polypeptide products

Patent: WO 0105974-A 43 25-JAN-2001;

Interleukin Genetics, Inc. (US)

FEATURES

Location/Qualifiers

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## RESULT 12

HS271338 6540 bp DNA linear PRI 18-APR-2002

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

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REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Location/Qualifiers

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Db 970 TGGAGAACAGGCAGACTCCACAGTCCCGCCAGGAGAA 1008

RESULT 13
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LOCUS
DEFINITION Homo sapiens interleukin-1 receptor antagonist homolog 1 (IL1HY1)
gene, complete cds.
ACCESSION AF216693
VERSION AF216693.1 GI:8572054
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 7604)
AUTHORS Mulero,J.J., Nelken,S.T. and Ford,J.E.
TITLE Organization of the human interleukin-1 receptor antagonist gene
IL1HY1
JOURNAL Immunogenetics 51 (6), 425-428 (2000)
MEDLINE 20322477
PUBMED 10866108
REFERENCE
2 (bases 1 to 7604)
AUTHORS Mulero,J.J., Nelken,S.T. and Ford,J.E.
TITLE Direct Submission
JOURNAL Submitted (15-DEC-1999) Functional Genomics, HYSEQ Inc, 670 Almaror
Ave., Sunnyvale, CA 94086, USA
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Best Local Similarity 97.4%; Pred. No. 0.00087;
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LOCUS
DEFINITION A novel interleukin-1 receptor antagonist and uses thereof.
ACCESSION BD211437
VERSION BD211437.1 GI:33021207
KEYWORDS JP 2002510492-A/6.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 7605)
AUTHORS Ford,J. and Pace,A.
TITLE A novel interleukin-1 receptor antagonist and uses thereof
JOURNAL Patent: JP 2002510492-A 6 09-APR-2002;
HYSEQ INC
COMMENT
OS Homo sapiens (human)
PN JP 2002510492-A/6
PD 09-APR-2002
PF 05-APR-1999 JP 2000542457
PR 03-APR-1998 US 09/055010,15-MAY-1998 US 09/079909 PR
20-MAY-1998 US 09/082364,19-JUN-1998 US 09/099818 PR
31-JUL-1998 US 09/127698,13-JAN-1999 US 09/229591 PR
17-FEB-1999 US 09/251370
PI JOHN FORD, ANN PACE
PC C12N15/09,A61K39/00,C07K14/52,C07K16/24,C12N1/15,
PC C12N1/19,
PC C12N1/21,C12N5/10,C12Q1/68,G01N33/50,G01N33/566,G01N33/68, PC
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GenCore version 5.1.6  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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AC AAF27921;  
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DT 08-MAY-2001 (first entry)  
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DE Human IL-IL1 coding sequence.  
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KW Human; IL-IL1; interleukin-1 locus; IL-1beta; IL-1receptor; psoriasis;  
KW chromosome 2q13; inflammatory disease; heart disease; Graves' disease;  
KW rheumatoid arthritis; inflammatory bowel disorder; diabetes; cancer;  
KW osteoporosis; systemic lupus erythematosus; ss.  
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OS Homo sapiens.  
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FH Key Location/Qualifiers  
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FT /note= "this region is specifically claimed"

WO200105974-A2.

25-JAN-2001.

17-JUL-2000; 2000WO-US019508.

16-JUL-1999; 99US-0144298P.

(INTE-) INTERLEUKIN GENETICS INC.

PI Nicklin M, Barton J;

DR WPI; 2001-091974/10.

PT Nucleic acids encoding human and murine interleukin-IL1 polypeptides  
PT useful for controlling inflammatory processes.

PS Claim 12; Fig 1; 150pp; English.

CC The present invention provides the protein and coding sequences of the

CC human and murine interleukin-IL1 (IL-IL1) proteins. The IL-IL1 gene is  
CC located between the IL-1beta and IL-1receptor genes at human chromosome  
CC 2q13. The sequences are useful in the diagnosis, prevention and treatment  
CC of heart disease, cancer and inflammatory diseases such as rheumatoid  
CC arthritis, systemic lupus erythematosus, inflammatory bowel disorder,  
CC diabetes, psoriasis, osteoporosis, lichen sclerosis, ulcerative colitis,  
CC severe periodontal disease and pregnancy complications. The present  
CC sequence is the human IL-IL1 coding sequence  
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DB 901 CTTCTCACTCACCACCTGTGCGAGAGAGGAGGTGGTCAATAGAGTCAGGAGTCTATGGCCCT 960  
QY 961 TGGCCCGAGCCCAACCCCTTCCCTTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
DB 961 TGGCCCGAGCCCAACCCCTTCCCTTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
QY 1021 CTTCTCTCATCATCTGTTGTTGGGCATGAGGAGGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
DB 1021 CTTCTCTCATCATCTGTTGTTGGGCATGAGGAGGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
QY 1081 GCTCAGAGCAATAAAGATAAGTATGCTGATCTCTCTTTTAAACCCCAAGATACAA 1140  
DB 1081 GCTCAGAGCAATAAAGATAAGTATGCTGATCTCTCTTTTAAACCCCAAGATACAA 1140  
QY 1141 TCAAAATCCAGATGCTGCTCTATTTCCCATGAAAAAGTGTCTCATGATATTGAGAAG 1200  
DB 1141 TCAAAATCCAGATGCTGCTCTATTTCCCATGAAAAAGTGTCTCATGATATTGAGAAG 1200  
QY 1201 ACCTACTTCAAAAGTGGGCATATATTGCAATTTTAAATTAAGAGATACCTATTATAT 1260  
DB 1201 ACCTACTTCAAAAGTGGGCATATATTGCAATTTTAAATTAAGAGATACCTATTATAT 1260  
QY 1261 ATTTCTTTATAGAAAAAGTCTGGAAGAGTGTACTTCAATTTAGCAATTTGTCAGGCTGT 1320  
DB 1261 ATTTCTTTATAGAAAAAGTCTGGAAGAGTGTACTTCAATTTAGCAATTTGTCAGGCTGT 1320  
QY 1321 GGCAGTATAGGTGATTTTCTTTTAAATTTATTTATTTATTTCTTCTTCTTCTTCTTCTTCT 1380  
DB 1321 GGCAGTATAGGTGATTTTCTTTTAAATTTATTTATTTATTTCTTCTTCTTCTTCTTCTTCT 1380  
QY 1381 ACAATGAAGTCAATTTCTTGTATTAATAAGAAAGAAATTAATCTTGAGTAGCAG 1440  
DB 1381 ACAATGAAGTCAATTTCTTGTATTAATAAGAAAGAAATTAATCTTGAGTAGCAG 1440  
QY 1441 AGCAGACATCATCTCTGATTGCTCAGCTCCCAATTTCCCGAGAGTAAATTTCAAAATTGAA 1500  
DB 1441 AGCAGACATCATCTCTGATTGCTCAGCTCCCAATTTCCCGAGAGTAAATTTCAAAATTGAA 1500  
QY 1501 TCGAGCTCTGCTGCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1560  
DB 1501 TCGAGCTCTGCTGCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1560  
QY 1561 ACTGAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620  
DB 1561 ACTGAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620  
QY 1621 AACAAAAATCATCTGTTAAATTTCTTCTAGAGGATCACAGCCCTGGGATTTCCAGGCA 1680  
DB 1621 AACAAAAATCATCTGTTAAATTTCTTCTAGAGGATCACAGCCCTGGGATTTCCAGGCA 1680  
QY 1681 TTGGATTCAGTCTCTAAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740  
DB 1681 TTGGATTCAGTCTCTAAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740  
QY 1741 ATCCCTCTTGGATCTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800  
DB 1741 ATCCCTCTTGGATCTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800  
QY 1801 TAGTTAAGAACAAAGGTCTATGCTGATGAAGGTAGACCTAAATTTCAATATGACTGGTTTCTCT 1860  
DB 1801 TAGTTAAGAACAAAGGTCTATGCTGATGAAGGTAGACCTAAATTTCAATATGACTGGTTTCTCT 1860  
QY 1861 TGTATGAAAGAGAGGACACAGACAGAGGAGCGCGGGGAAGACTATGTAAAGATGA 1920  
DB 1861 TGTATGAAAGAGAGGACACAGACAGAGGAGCGCGGGGAAGACTATGTAAAGATGA 1920  
QY 1921 AGGCGAGATCGAGTCTTGGAGCCACAGCTTAAGAAACACCAAGATTTGTCGCAACCAT 1980  
DB 1921 AGGCGAGATCGAGTCTTGGAGCCACAGCTTAAGAAACACCAAGATTTGTCGCAACCAT 1980

QY 1981 CAGAAGCTTGGAGAGGCAAGAGAAATCTTCCCTAGAGGCTTTAGAGGGATAACGGCT 2040  
DB 1981 CAGAAGCTTGGAGAGGCAAGAGAAATCTTCCCTAGAGGCTTTAGAGGGATAACGGCT 2040  
QY 2041 CTGCTGAAACCTTAATCTCAGACTCTCAGCCTCTGAAAGAGAAAGAAATAAATTCGGC 2100  
DB 2041 CTGCTGAAACCTTAATCTCAGACTCTCAGCCTCTGAAAGAGAAAGAAATAAATTCGGC 2100  
QY 2101 TGTGTTAAGCCACCAAGGATAATGTTGTTACAGAGCTCTAGGAACTAATACAGCTGCTA 2160  
DB 2101 TGTGTTAAGCCACCAAGGATAATGTTGTTACAGAGCTCTAGGAACTAATACAGCTGCTA 2160  
QY 2161 AAATGATCCTGCTCTCTGTTTACATCTGTGTGTGTCCTCCCAATGTACCAA 2220  
DB 2161 AAATGATCCTGCTCTCTGTTTACATCTGTGTGTGTCCTCCCAATGTACCAA 2220  
QY 2221 AGTTGCTTTGTTGACCAATAGAAATATGAGAGAGTGGATGCACTTCCAAGATTA 2280  
DB 2221 AGTTGCTTTGTTGACCAATAGAAATATGAGAGAGTGGATGCACTTCCAAGATTA 2280  
QY 2281 GGTATAAAGACACTGACGCTTCTACTTGAGCCCTCTCTCTGCCACCCACCGCCCC 2340  
DB 2281 GGTATAAAGACACTGACGCTTCTACTTGAGCCCTCTCTCTGCCACCCACCGCCCC 2340  
QY 2341 AATCTATCTTGCTGCTCTGCTCTGGGGAAGCTAGTGCCTATGAGCAGGCTAT 2400  
DB 2341 AATCTATCTTGCTGCTCTGCTCTGGGGAAGCTAGTGCCTATGAGCAGGCTAT 2400  
QY 2401 AAAGAGACTTACGTGTTAAATGAAGTCTCTGCCACAGCCACATTAAGTGAACCTAG 2460  
DB 2401 AAAGAGACTTACGTGTTAAATGAAGTCTCTGCCACAGCCACATTAAGTGAACCTAG 2460  
QY 2461 AAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTAAAGTTGCTCAGTTTGTCTA 2520  
DB 2461 AAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTAAAGTTGCTCAGTTTGTCTA 2520  
QY 2521 ACTTGTTATGAGCAATAGATAAATAATATGAGAGAAAGAG 2562  
DB 2521 ACTTGTTATGAGCAATAGATAAATAATATGAGAGAAAGAG 2562

RESULT 2  
AAF92133  
ID AAF92133 standard; cDNA; 2598 BP.

AC AAF92133;  
DT 15-MAY-2001 (first entry)  
DE Human PRO4342 cDNA.  
XX Human; PRO protein; mapping; ss.  
XX Homo sapiens.  
OS WO200116318-A2.  
PN 08-MAR-2001.  
XX 24-AUG-2000; 2000WO-US023328.  
XX 01-SEP-1999; 99WO-US020111.  
PR 15-SEP-1999; 99WO-US021090.  
PR 07-DEC-1999; 99US-0169495P.  
PR 09-DEC-1999; 99US-0170262P.  
PR 11-JAN-2000; 2000US-0175481P.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 03-MAR-2000; 2000US-0187202P.  
PR 21-MAR-2000; 2000US-0191007P.

PR 10-MAR-2000; 2000WO-US008439.  
PR 25-APR-2000; 2000US-0199397P.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 05-JUN-2000; 2000US-0209832P.  
XX (GETH ) GENENTECH INC.  
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;  
XX WPI; 2001-183260/18.  
DR P-PSDB; AAB87601.  
XX Eighty four nucleic acids encoding PRO polypeptides, useful in molecular  
PT biology, including use as hybridization probes, and in chromosome and  
PT gene mapping.  
XX Claim 2; Fig 151; 278pp; English.  
XX The present sequence is the coding sequence for a human PRO polypeptide  
CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO  
CC antagonists or anti-PRO antibodies are useful for preparation of a  
CC medicament useful in the treatment of a condition which is responsive to  
CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO  
CC protein may also be employed as molecular weight markers for protein  
CC electrophoresis. The PRO coding sequence has applications in molecular  
CC biology, including use as hybridisation probes, and in chromosome and  
CC gene mapping  
XX Sequence 2598 BP; 687 A; 590 C; 648 G; 673 T; 0 U; 0 Other;

Query Match 98.1%; Score 2514.2; DB 4; Length 2598;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 2552; Conservative 0; Mismatches 8; Indels 3; Gaps 3;  
QY 1 AGGGAGCTACACCTGTGGAGCTCAGATCGTCTGAGTGGGGCGCTGCTCCGAA 60  
DB 38 AGGGAGCTACACCTGTGGAGCTCAGATCGTCTGAGTGGGGCGCTGCTCCGAA 97  
QY 61 TGAAGGACTTCGGCAATTGAAGGTGCTTTATCTGCATAATAACCAAGCTTCTAGCTGGAGGC 120  
DB 98 TGAAGGACTTCGGCAATTGAAGGTGCTTTATCTGCATAATAACCAAGCTTCTAGCTGGAGGC 157  
QY 121 TGCATCGAGGGAAGGTCAATTAAGGTGAAGAGATCAGCGTGTCCCAATCGGTGCTGG 180  
DB 158 TGCATCGAGGGAAGGTCAATTAAGGTGAAGAGATCAGCGTGTCCCAATCGGTGCTGG 217  
QY 181 ATGCCAGCTGTCCCGCTCATCTGGGTGTCAGGGTGGAGCCAGTCCCTGTCATG 240  
DB 218 ATGCCAGCTGTCCCGCTCATCTGGGTGTCAGGGTGGAGCCAGTCCCTGTCATG 277  
QY 241 GGGTGGGCGAGGAGCGACTCTAACACTAGAGCCAGTGAACATCATGAGCTCTATCTTG 300  
DB 278 GGGTGGGCGAGGAGCGACTCTAACACTAGAGCCAGTGAACATCATGAGCTCTATCTTG 337  
QY 301 GTGCCAAGGAATCCAAAGCTTCACTTCTACCGGGGACATGCGGCTCACTCCAGCT 360  
DB 338 GTGCCAAGGAATCCAAAGCTTCACTTCTACCGGGGACATGCGGCTCACTCCAGCT 397  
QY 361 TCGAGTCCGCTGCTTACCGGGGCTGGTCTCTGTCACCGTGTGAGCCGATCAGCCTG 420  
DB 398 TCGAGTCCGCTGCTTACCGGGGCTGGTCTCTGTCACCGTGTGAGCCGATCAGCCTG 457  
QY 421 TCAGACTCACCAGCTTCCCGAGAAATGGTGGTGGAAATGCCCCCATCACAGACTTCTACT 480  
DB 458 TCAGACTCACCAGCTTCCCGAGAAATGGTGGTGGAAATGCCCCCATCACAGACTTCTACT 517  
QY 481 TCCAGCAGTGTGACTAGGGCAACGTCGCCCCCCAGAACTCCCTGGGAGAGCCAGCTCGG 540  
DB 518 TCCAGCAGTGTGACTAGGGCAACGTCGCCCCCCAGAACTCCCTGGGAGAGCCAGCTCGG 576  
QY 541 GTGAGGGTGTGAGGAGAGACCCATGCGGGAATCACTCTTCTGCTCTCAGNACCCC 600

Db 577 GTGAGGGTGTGAGTGGAGGAGACCCATGGCGGACAAATCACTCTCTGTCTCTCAGGACCCC 636  
QY 601 CAGGCTGTGACTTAGTGGGACCTGACCACTTTGTCTTCTGTTCCAGTTTCATAAATT 660  
Db 637 CAGCTGTGACTTAGTGGGACCTGACCACTTTGTCTTCTGTTCCAGTTTCATAAATT 696  
QY 661 CTGAGATTTGGAGCTCAGTCCAGGTCCTCCCCCACTGGATGGTGTCTACTGTCTGGAAC 720  
Db 697 CTGAGATTTGGAGCTCAGTCCAGGTCCTCCCCCACTGGATGGTGTCTACTGTCTGGAAC 756  
QY 721 CTTGTAAAAACCAATGTGGGGTAAATGGGAATAACATGAAGAAATTTCTGTGGGGTGG 780  
Db 757 CTTGTAAAAACCAATGTGGGGTAAATGGGAATAACATGAAGAAATTTCTGTGGGGTGG 816  
QY 781 GTGGGGAGTGTGGGAATCAATTCCTGCTTAATGGTAACTGACAGTGTATCACTCGAGCC 840  
Db 817 GTGGGGAGTGTGGGAATCAATTCCTGCTTAATGGTAACTGACAGTGTATCACTCGAGCC 876  
QY 841 CCGCAGGCCAACCCATCCCCAGTTGAGCCCTTATAGGCTCAGTAGCTCTCCACATGAAGTC 900  
Db 877 CCGCAGGCCAACCCATCCCCAGTTGAGCCCTTATAGGCTCAGTAGCTCTCCACATGAAGTC 936  
QY 901 CTCTCACTCACTGTGACGAGAGAGGAGTGGTCAATAGAGTCAGGGATCTATGGCCCT 960  
Db 937 CTGTCACTCACTGTGACGAGAGAGGAGTGGTCAATAGAGTCAGGGATCTATGGCCCT 996  
QY 961 TGGCCAGCCGCCACCCCTTCCCTTT - ATCCCTGCCACTGTCAATGCTACCTTTCCCTATC 1019  
Db 997 TGGCCAGCCGCCACCCCTTCCCTTTAATCCTGCCACTGTCAATGCTACCTTTCCCTATC 1056  
QY 1020 TCTTCCCTCATCATCTTGTGTGGGCATGAGGAGTGGTGAATCTCAGAGAAATGGTTCCG 1079  
Db 1057 TCTTCCCTCATCATCTTGTGTGGGCATGAGGAGTGGTGAATCTCAGAGAAATGGTTCCG 1116  
QY 1080 AGCTCAGAGATAAAGATAGTAGGATGCTGATCCCTTTTAAAAACCCAGATACA 1139  
Db 1117 AGCTCAGAGATAAAGATAGTAGGATGCTGATCCCTTTTAAAAACCCAGATACA 1176  
QY 1140 ATCAATATCCAGATGCTGCTCTATTCCCATGAAAAAGTGTCAATGACATATCAGAA 1199  
Db 1177 ATCAATATCCAGATGCTGCTCTATTCCCATGAAAAAGTGTCAATGACATATCAGAA 1236  
QY 1200 GACCTACTTCAAGTGGCATAATATGCAATTTATTTTAAATTAAGATACCTATTATTA 1259  
Db 1237 GACCTACTTCAAGTGGCATAATATGCAATTTATTTTAAATTAAGATACCTATTATTA 1296  
QY 1260 TATTTCTTTATAGAAAAAGTGTGGAAGTGTACTTCAATGTCGAATGTCAAGGTGG 1319  
Db 1297 TATTTCTTTATAGAAAAAGTGTGGAAGTGTACTTCAATGTCGAATGTCAAGGTGG 1356  
QY 1320 TGGCAGTATAGGTGATTTTCTTTTAAATCTGTGTTAATTTATCTGATTTTCTTAATTTTC 1379  
Db 1357 TGGCAGTATAGGTGATTTTCTTTTAAATCTGTGTTAATTTATCTGATTTTCTTAATTTTC 1416  
QY 1380 TACAATGAAGATGAATTTCTTTGTATAAAAAATAAGAAAGAAATTAATCTTTGAGGTAGCA 1439  
Db 1417 TACAATGAAGATGAATTTCTTTGTATAAAAAATAAGAAAGAAATTAATCTTTGAGGTAGCA 1476  
QY 1440 GAGCAGACATCATCTCTGATGCTCCTCAGCTCAATTTCCCGAGATTAATTCATAATGA 1499  
Db 1477 GAGCAGACATCATCTCTGATGCTCCTCAGCTCCTCAGCTCCTCAGAGTAAATTTCAATTTGA 1536  
QY 1500 ATCCAGCTCTGCTCTCTGTTGTTGTTGTAGTAGTATCAGAGAAACAGATCTCAGCAAGC 1559  
Db 1537 ATCCAGCTCTGCTCTCTGTTGTTGTTGTAGTAGTATCAGAGAAACAGATCTCAGCAAGC 1596  
QY 1560 CACTGAGGAGGAGCTGTGCTGAGTGTGTGGCTGGAAATCTCTGGGTAAAGAACTTAAA 1619  
Db 1597 CACTGAGGAGGAGCTGTGCTGAGTGTGTGGCTGGAAATCTCTGGGTAAAGAACTTAAA 1656  
QY 1620 GAAACAAAATCATCTGGTAATTTCTTCTAGAGGATCAGAGCCCTGGGATTCAGAGGC 1679  
Db 1657 GAAACAAAATCATCTGGTAATTTCTTCTAGAGGATCAGAGCCCTGGGATTCAGAGGC 1716

QY 1680 ATTGGATCCAGTCTCTAAGAAAGGCTGTGTACTGTTGTAATTTGTGTCCCTCCTCAAAATCA 1739  
Db 1717 ATTGGATCCAGTCTCTAAGAAAGGCTGTGTACTGTTGTAATTTGTGTCCCTCCTCAAAATCA 1776  
QY 1740 CATCTCTTCTGGAATCTCAGTCTGTGAGTTTATTTGGAGATAAGGTCTCTGCAGATGTAG 1799  
Db 1777 CATCTCTTCTGGAATCTCAGTCTGTGAGTTTATTTGGAGATAAGGTCTCTGCAGATGTAG 1836  
QY 1800 TTAGTTAAGACAAGTCTATGCTGATGAAGGTAGACCTTAAATTTCAATATGACTGTTTCC 1859  
Db 1837 TTAGTTAAGACAAGTCTATGCTGATGAAGGTAGACCTTAAATTTCAATATGACTGTTTCC 1896  
QY 1860 TTGTATGAAAAAGGAGAGACACAGAGACAGAGAGACGCGGGGAAGACTATGTAAAGATG 1919  
Db 1897 TTGTATGAAAAAGGAGAGACACAGAGACAGAGAGACGCGGGGAAGACTATGTAAAGATG 1956  
QY 1920 AAGGACAGATCGGAGTTTTCAGCCCAAGCTAAGAAACACCAAGGATTCGTGGCAACA 1979  
Db 1957 AAGGACAGATCGGAGTTTTCAGCCCAAGCTAAGAAACACCAAGGATTCGTGGCAACA 2016  
QY 1980 TCAGAAAGCTTGAAGAGGCAAAAGAAATTTCTTCCCTAGAGGCTTTAGAGGATAACGCG 2039  
Db 2017 TCAGAAAGCTTGAAGAGGCAAAAGAAATTTCTTCCCTAGAGGCTTTAGAGGATAACGCG 2076  
QY 2040 TCTGCTGAAACCTTAATCTCAGACTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAG 2099  
Db 2077 TCTGCTGAAACCTTAATCTCAGACTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAG 2136  
QY 2100 CTGTTTAAAGCCCAAGGATAATTTGTTACAGAGCTCTAGGAACTTAATACAGCTGCT 2159  
Db 2137 CTGTTTAAAGCCCAAGGATAATTTGTTACAGAGCTCTAGGAACTTAATACAGCTGCT 2196  
QY 2160 AAAATGATCCCTGTCTCTCTGTTTACATTTCTGTGTGTGCTCCCTCCCAATGTACCA 2219  
Db 2197 AAAATGATCCCTGTCTCTCTGTTTACATTTCTGTGTGTGCTCCCTCCCAATGTACCA 2256  
QY 2220 AAGTTGTCTTTGTGACCCAAATAGAAATATGGCAAGATGATGGCATGCCACTTCCAGATTT 2279  
Db 2257 AAGTTGTCTTTGTGA - CCAATAGAAATATGGCAAGATGATGGCATGCCACTTCCAGATTT 2315  
QY 2280 AGTTTATAAAGACACTGCAGCTTCTACTTGAGCCCTCTCTCTGCGCAACCCACCCGCC 2339  
Db 2316 AGTTTATAAAGACACTGCAGCTTCTACTTGAGCCCTCTCTCTGCGCAACCCACCCGCC 2375  
QY 2340 CAATCTATCTTGGCTCAGTCTCTGCGCTCTGGGGGAAGTGTGCTGCAATGTAGAGAGGCTTA 2399  
Db 2376 CAATCTATCTTGGCTCAGTCTCTGCGCTCTGGGGGAAGTGTGCTGCAATGTAGAGAGGCTTA 2435  
QY 2400 TAAAGAGACTTACGTGGTAAATAATGAAGTCTCCCTGCCACAGCCACATTAGTGAACTTA 2459  
Db 2436 TAAAGAGACTTACGTGGTAAATAATGAAGTCTCCCTGCCACAGCCACATTAGTGAACTTA 2495  
QY 2460 GAAGCAGACACTCTGTGAGATAATCGATGTTTGTGTTTAAAGTGTCTCAGTTTGGTCT 2519  
Db 2496 GAAGCAGACACTCTGTGAGATAATCGATGTTTGTGTTTAAAGTGTCTCAGTTTGGTCT 2555  
QY 2520 AACTTGTATGAGCAATAGATAAATAATATCCAGAGAAAGAG 2562  
Db 2556 AACTTGTATGAGCAATAGATAAATAATATCCAGAGAAAGAG 2598

RESULT 3

ABS74453  
ID ABS74453 standard; cDNA; 2598 BP.

XX ABS74453;

AC ABS74453;

XX 10-DEC-2002 (first entry)

XX Human cDNA encoding secreted/transmembrane protein PRO4342.

XX Human; ss; gene; secreted protein; transmembrane protein; antirheumatic;

KW antiarthritic; osteopathic; sports-related joint problem;  
KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.

XX Homo sapiens.

XX US2002119130-A1.

XX 29-AUG-2002.

XX 06-DEC-2001; 2001US-00008667.

XX 29-OCT-1997; 97US-0063435P.

XX 29-OCT-1997; 97US-0064215P.

XX 22-APR-1998; 98US-0082797P.

XX 29-APR-1998; 98US-0083495P.

XX 02-MAY-1998; 98US-0085579P.

XX 02-JUN-1998; 98US-0087759P.

XX 04-JUN-1998; 98US-0088021P.

XX 04-JUN-1998; 98US-0088029P.

XX 04-JUN-1998; 98US-0088030P.

XX 10-JUN-1998; 98US-0088734P.

XX 10-JUN-1998; 98US-0088740P.

XX 10-JUN-1998; 98US-0088811P.

XX 10-JUN-1998; 98US-0088824P.

XX 10-JUN-1998; 98US-0088825P.

XX 11-JUN-1998; 98US-0088863P.

XX 12-JUN-1998; 98US-0089105P.

XX 16-JUN-1998; 98US-0089514P.

XX 17-JUN-1998; 98US-0089553P.

XX 19-JUN-1998; 98US-0089552P.

XX 22-JUN-1998; 98US-0090246P.

XX 24-JUN-1998; 98US-0090444P.

XX 25-JUN-1998; 98US-0090688P.

XX 25-JUN-1998; 98US-0090696P.

XX 26-JUN-1998; 98US-0090862P.

XX 02-JUL-1998; 98US-0091828P.

XX 10-AUG-1998; 98US-00956012P.

XX 17-AUG-1998; 98US-0096757P.

XX 18-AUG-1998; 98US-0096949P.

XX 18-AUG-1998; 98US-0096959P.

XX 26-AUG-1998; 98US-0097954P.

XX 26-AUG-1998; 98US-0097971P.

XX 26-AUG-1998; 98US-0097979P.

XX 01-SEP-1998; 98US-0098749P.

XX 10-SEP-1998; 98US-0099741P.

XX 10-SEP-1998; 98US-0099763P.

XX 10-SEP-1998; 98US-0099792P.

XX 10-SEP-1998; 98US-0099812P.

XX 10-SEP-1998; 98US-0099815P.

XX 16-SEP-1998; 98US-0100627P.

XX 16-SEP-1998; 98US-0100627P.

XX 17-SEP-1998; 98US-01019330.

XX 17-SEP-1998; 98US-0100863P.

XX 17-SEP-1998; 98US-0100864P.

XX 17-SEP-1998; 98US-0100330P.

XX 22-SEP-1998; 98US-0101279P.

XX 23-SEP-1998; 98US-0101475P.

XX 24-SEP-1998; 98US-0101738P.

XX 24-SEP-1998; 98US-0101743P.

XX 24-SEP-1998; 98US-0101916P.

XX 30-SEP-1998; 98US-0102570P.

XX 06-OCT-1998; 98US-0103449P.

XX 08-MAR-1999; 98US-0005028P.

XX 14-MAY-1999; 99WO-US010733.

XX 02-JUN-1999; 99WO-US012252.

XX 01-SEP-1999; 99WO-US020111.

XX 15-SEP-1999; 99WO-US021090.

XX 22-DEC-1999; 99WO-US021194.

XX 18-FEB-2000; 2000WO-US004341.

XX 18-FEB-2000; 2000WO-US004342.

XX 22-FEB-2000; 2000WO-US004414.

XX 01-MAR-2000; 2000WO-US005601.

PR 30-MAR-2000; 2000WO-US008439.

PR 22-MAY-2000; 2000WO-US014042.

PR 02-JUN-2000; 2000WO-US015264.

PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.

PR 10-NOV-2000; 2000WO-US030873.

PR 01-DEC-2000; 2000WO-US032378.

PR 20-DEC-2000; 2000WO-US034956.

PR 28-FEB-2001; 2001WO-US006520.

PR 01-MAR-2001; 2001WO-US006666.

PR 30-MAY-2001; 2001WO-US017443.

PR 01-JUN-2001; 2001WO-US017800.

PR 20-JUN-2001; 2001WO-US019692.

PR 09-JUL-2001; 2001WO-US021066.

XX 09-JUL-2001; 2001WO-US021735.

XX (GETH ) GENENTECH INC.

XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;

PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

XX WPI; 2002-731348/79.

XX P-PSDB; ABG95926.

XX New isolated secreted and transmembrane PRO polypeptide useful for

PT modulating biological activity of a cell, or for treating sports-related

PT joint problems, osteoarthritis or rheumatoid arthritis.

XX Claim 2; Fig 151; 399pp; English.

XX The invention relates to an isolated secreted and transmembrane PRO

CC polypeptide having 80 % sequence identity to a sequence appearing as

CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an

CC extracellular domain of the proteins with their associated signal peptide

CC or lacking its associated signal peptide. Also included are the nucleic

CC acids encoding the proteins, vectors, host cells, fusion proteins and

CC antibodies which specifically bind to the proteins. The proteins are

CC useful for detecting a polypeptide designated as A, B, C or D in a sample

CC suspected of containing an A, B, C or D polypeptide, by contacting the

CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)

CC and determining the formation of a A/E, B/F, C/G, H or I polypeptide

CC conjugate in the sample, where the formation of the conjugate is

CC indicative of the presence of an A, B, C or D polypeptide in the sample,

CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a

CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801

CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a

CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises

CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,

CC H or I polypeptide is labeled with a detectable label or is attached to a

CC solid support. The proteins are useful for linking a bioactive molecule

CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,

CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.

CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,

CC or I, or antibodies against them are useful for modulating a biological

CC activity of a cell expressing a polypeptide designated as A, B, C or D or

CC E, F, G, H, or I. The cell is killed. The proteins are useful for

CC identifying agonists or antagonists, for the preparation of a medicament

CC useful in the treatment of a condition which is responsive to the

CC proteins, as molecular weight markers for protein electrophoresis

CC purposes, and as therapeutic agents for treating sports-related joint

CC problems, articular cartilage defects, osteoarthritis or rheumatoid

CC arthritis. Nucleic acids encoding the proteins are useful as

CC hybridisation probes, in chromosome and gene mapping, in the generation

CC of anti-sense RNA and DNA, for the preparation of the proteins, to

CC generate transgenic or knockout animals which are useful in the

CC development and screening of therapeutic useful reagents, for chromosome

CC identification, and in gene therapy. The antibody is useful as a

CC therapeutic agent, in a diagnostic assay and for affinity purification of

CC the protein from recombinant cell culture natural sources. The present

CC invention encodes a novel secreted or transmembrane protein of the

CC invention

XX Sequence 2598 BP; 687 A; 590 C; 648 G; 673 T; 0 U; 0 Other;



Query Match 98.1%; Score 2514.2; DB 6; Length 2598; Best Local Similarity 99.6%; Pred. No. 0; Matches 2552; Conservative 0; Mismatches 8; Indels 3; Gaps 3;									
QY	1	AGGGAGCTTACACCTGTGGAGCTCAAGATGCTCTGATGGGGGGCGCTGTGCTCCGAA	60						
DB	38	AGGGAGCTTACACCTGTGGAGCTCAAGATGCTCTGATGGGGGGCGCTGTGCTCCGAA	97						
QY	61	TGAAGGACTCGGCATTGAAGTCTTTATCTGCATAATAACACAGCTTCTAGCTGGAGGCG	120						
DB	98	TGAAGGACTCGGCATTGAAGTCTTTATCTGCATAATAACACAGCTTCTAGCTGGAGGCG	157						
QY	121	TGCATCAGGGAAGGCTTAAAGGTGAAGAGATCAGCGTGGTCCCAATCGGTGGCTGG	180						
DB	158	TGCATCAGGGAAGGCTTAAAGGTGAAGAGATCAGCGTGGTCCCAATCGGTGGCTGG	217						
QY	181	ATGCCAGCTGTCCTCCGCTCATCTCGGTGTTCAGGGTGAAGCCAGTGCCTGCTCATGTG	240						
DB	218	ATGCCAGCTGTCCTCCGCTCATCTCGGTGTTCAGGGTGAAGCCAGTGCCTGCTCATGTG	277						
QY	241	GGGTGGGAGGAGCGGACTCTAACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG	300						
DB	278	GGGTGGGAGGAGCGGACTCTAACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG	337						
QY	301	GTGCCAAGGAATCCAAAGAGCTTCACTTCTACCGGCGGACATGGGGCTCACCTCCAGCT	360						
DB	338	GTGCCAAGGAATCCAAAGAGCTTCACTTCTACCGGCGGACATGGGGCTCACCTCCAGCT	397						
QY	361	TCAGTCTGGCTGCTACCGGGCTGGTCTCTGTGCAAGTGTCCGAGCGGATCAGCCTG	420						
DB	398	TCAGTCTGGCTGCTACCGGGCTGGTCTCTGTGCAAGTGTCCGAGCGGATCAGCCTG	457						
QY	421	TCAGACTCACCCAGCTTCCGAGAATGGGTGGGAAATGCCCAATCAAGACTTCTACT	480						
DB	458	TCAGACTCACCCAGCTTCCGAGAATGGGTGGGAAATGCCCAATCAAGACTTCTACT	517						
QY	481	TCAGAGTGTGACTAGGGCAACGTGCCCCCGGAGAACTCCCTGGGCGAGCCAGCTCGG	540						
DB	518	TCAGAGTGTGACTAGGGCAACGTG-CCCCCGAGAACTCCCTGGGCGAGCCAGCTCGG	576						
QY	541	GTGAGGGGTGAGTGAAGAGACCCATGGCGGCAATCACTCTTCTGTGCTCTAGGACCC	600						
DB	577	GTGAGGGGTGAGTGAAGAGACCCATGGCGGCAATCACTCTCTGTGCTCTAGGACCC	636						
QY	601	CAGGTCTGACTAGTGGGCACTGACCACTTCTTCTGTGTTCCAGTTTGCATAAAT	660						
DB	637	CAGGTCTGACTAGTGGGCACTGACCACTTCTTCTGTGTTCCAGTTTGGATAAAT	696						
QY	661	CTGAGATTTGGAGCTCAGTCCAGGGTCTCTCCCGCACTGGATGGTCTACTGTGGAAC	720						
DB	697	CTGAGATTTGGAGCTCAGTCCAGGGTCTCTCCCGCACTGGATGGTCTACTGTGGAAC	756						
QY	721	CTTGTAAAAACCATGTGGGTAACTGGGAATAACATGAAGAAATTTCTGTGGGGTGGG	780						
DB	757	CTTGTAAAAACCATGTGGGTAACTGGGAATAACATGAAGAAATTTCTGTGGGGTGGG	816						
QY	781	GTGGGGAGTGTGGGAATCATCTCTTAATGTTAACTGAAGTGTACCTTGAGCC	840						
DB	817	GTGGGGAGTGTGGGAATCATCTCTTAATGTTAACTGAAGTGTACCTTGAGCC	876						
QY	841	CCGAGGCCAAACCCATCCAGTTGAGCCTTATAGGGTCACTAGCTCTCCACATGAAGTC	900						
DB	877	CCGAGGCCAAACCCATCCAGTTGAGCCTTATAGGGTCACTAGCTCTCCACATGAAGTC	936						
QY	901	CTCTCACTCACTGTGAGGAGAGGGAGTGGTCAAGTCAAGGATCTATAGCCCT	960						
DB	937	CTGTCACTCACTGTGAGGAGAGGGAGTGGTCAAGTCAAGGATCTATAGCCCT	996						
QY	961	TGGCCAGCCGCCACCCCTTCCCTTT-ATCCTGCACTGTCTATGCTACCTTCCCTATC	1019						
DB	997	TGGCCAGCCGCCACCCCTTCCCTTTAATCTCTGCCACTGTCTATGCTACCTTCTCTATC	1056						
QY	1020	TCCTCCCTCATCATCTTGTGTGGGATGAGAGGTGGTGTGATGTGATGATGATGATGATGATG	1079						
DB	1057	TCCTCCCTCATCATCTTGTGTGGGATGAGAGGTGGTGTGATGTGATGATGATGATGATG	1116						
QY	1080	AGCTCAGAAGATAAAGATAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG	1139						
DB	1117	AGCTCAGAAGATAAAGATAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG	1176						
QY	1140	ATCAAAATCCAGATGCTGCTCTATTTCCCATGAAAAGTGTCTCATGATATATTTGAGAA	1199						
DB	1177	ATCAAAATCCAGATGCTGCTCTATTTCCCATGAAAAGTGTCTCATGATATATTTGAGAA	1236						
QY	1200	GACCTATTACAAAGTGGCATATATTTGCAATTTATTTAAATTTAAAGATACCTATTTATA	1259						
DB	1237	GACCTATTACAAAGTGGCATATATTTGCAATTTATTTAAATTTAAAGATACCTATTTATA	1296						
QY	1260	TATTTCTTTATAGAAAAGTCTGGAAGTGTCTCAATTTGTAGCAATGTGCAATGTGCAATGTG	1319						
DB	1297	TATTTCTTTATAGAAAAGTCTGGAAGTGTCTCAATTTGTAGCAATGTGCAATGTGCAATGTG	1356						
QY	1320	TGCGAGTATAGTGTGATTTTCTTTTAAATTTCTGTAAATTTATCTGTATTTCTTAAATTTTC	1379						
DB	1357	TGCGAGTATAGTGTGATTTTCTTTTAAATTTCTGTAAATTTATCTGTATTTCTTAAATTTTC	1416						
QY	1380	TACAATGAAGATGAATCTCTGTATATAAATAAAGAAAAGAAATTAATCTTGAGGTAAAGCA	1439						
DB	1417	TACAATGAAGATGAATCTCTGTATATAAATAAAGAAAAGAAATTAATCTTGAGGTAAAGCA	1476						
QY	1440	GAGCAGACATCATCTGATGCTCTGAGCTCCAAATTTCCCGCAGAGTAAATTTCAAAATCA	1499						
DB	1477	GAGCAGACATCATCTGATGCTCTGAGCTCCAAATTTCCCGCAGAGTAAATTTCAAAATCA	1536						
QY	1500	ATCGAGCTCTGCTGCTCTGCTGTTGTTAGTAGTGTGATGATGATGATGATGATGATGATG	1559						
DB	1537	ATCGAGCTCTGCTGCTCTGCTGTTGTTAGTAGTGTGATGATGATGATGATGATGATG	1596						
QY	1560	CATCGAGGAGGCTGCTGCTGATGTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1619						
DB	1597	CATCGAGGAGGCTGCTGCTGATGTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1656						
QY	1620	GAACAAATCATCTGTTAAATTTCTCTAGAGATGATGATGATGATGATGATGATGATGATG	1679						
DB	1657	GAACAAATCATCTGTTAAATTTCTCTAGAGATGATGATGATGATGATGATGATGATGATG	1716						
QY	1680	ATTGATCAGTCTCTAAGAGGCTGCTGATCTGTTGATTTGTTGTTGTTGTTGTTGTTGTTG	1739						
DB	1717	ATTGATCAGTCTCTAAGAGGCTGCTGATCTGTTGATTTGTTGTTGTTGTTGTTGTTGTTG	1776						
QY	1740	CATCTCTTTGGAATCTCAGTCTGTGATTTATTTGGAGATAGGTCTCTGAGATGTAG	1799						
DB	1777	CATCTCTTTGGAATCTCAGTCTGTGATTTATTTGGAGATAGGTCTCTGAGATGTAG	1836						
QY	1800	TTAGTTAAGACAGGTCTGCTGGATGAGGTAGACCTTAAATTTCAATGATGATGATGATG	1859						
DB	1837	TTAGTTAAGACAGGTCTGCTGGATGAGGTAGACCTTAAATTTCAATGATGATGATGATG	1896						
QY	1860	TTGTATGAAAAGCAGACACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGAC	1919						
DB	1897	TTGTATGAAAAGCAGACACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGAC	1956						
QY	1920	AAGGAGAGATCGGAGTTTTCAGCCACCAAGCTAAGAAACACCAAGGATTTGGCAACCA	1979						
DB	1957	AAGGAGAGATCGGAGTTTTCAGCCACCAAGCTAAGAAACACCAAGGATTTGGCAACCA	2016						
QY	1980	TCAGAGCTTGAAGAGGCAAGAAATTTCTTCCCTAGAGCTTTAGAGGATACCGC	2039						
DB	2017	TCAGAGCTTGAAGAGGCAAGAAATTTCTTCCCTAGAGCTTTAGAGGATACCGC	2076						
QY	2040	TCGTCTGAAACCTTAAATCTCAGACTTCCAGCTCTCTGAAACGAAAGAAATTTAAATTC	2099						
DB	2077	TCGTCTGAAACCTTAAATCTCAGACTTCCAGCTCTCTGAAACGAAAGAAATTTAAATTC	2136						
QY	2100	CTGTTTAAAGCCCAAGGATTAATTTGTTTACAGAGCTCTAGGAAACTTAATACAGCTGCT	2159						

[illegible]

QY 241 GGGTGGGCGAGCGGACTCTAAACATAGAGCAGTGAACATCATGGAGCTCTATCTTG 300  
Db |||||  
QY 278 GGGTGGGCGAGGAGCGACTCTAAACATAGAGCAGTGAACATCATGGAGCTCTATCTTG 337  
Db |||||  
QY 301 GTGCCAAGGAATCCAAAGAGCTTACCTTCTACCGGCGGACATGGGGTCTACCTCCAGCT 360  
Db |||||  
QY 338 GTGCCAAGGAATCCAAAGAGCTTACCTTCTACCGGCGGACATGGGGTCTACCTCCAGCT 397  
QY 361 TCAGTCTGGCTGCTACCGGGGCTGTTCTGTGACAGGTGCTGTAAGCCGATCAGCCTG 420  
Db |||||  
QY 398 TCAGTCTGGCTGCTACCGGGGCTGTTCTGTGACAGGTGCTGTAAGCCGATCAGCCTG 457  
QY 421 TCAGTCTACCGAGCTTCCCGAGAAATGGTGGTGGAAATGCCCCATCAGAGCTTCTACT 480  
Db |||||  
QY 458 TCAGTCTACCGAGCTTCCCGAGAAATGGTGGTGGAAATGCCCCATCAGAGCTTCTACT 517  
QY 481 TCAGAGTGTGTACTAGGCGAACGTGCCCCGCCAGAAATCCCTGGGCGAGCGAGCTCGG 540  
Db |||||  
QY 518 TCAGAGTGTGTACTAGGCGAACGTG-CGCCCCAGAACTCCCTGGGCGAGCGAGCTCGG 576  
QY 541 GTAGGGGTGAGTGGAGAGACCCATGGCGGACAACTCACTTCTGCTCTCAGGACCCC 600  
Db |||||  
QY 577 GTAGGGGTGAGTGGAGAGACCCATGGCGGACAACTCACTTCTGCTCTCAGGACCCC 636  
QY 601 CAGGTCTGACTTGTAGTGGGCACTGACCACTTGTCTTCTGTTTCCAGTGTTCGATAAAT 660  
Db |||||  
QY 637 CAGGTCTGACTTGTAGTGGGCACTGACCACTTGTCTTCTGTTTCCAGTGTTCGATAAAT 696  
QY 661 CTGAGATTTGGAGCTCAGTCCAGGTCCTCCGCCACTGGATGGTGTCTGCTGTGGAAC 720  
Db |||||  
QY 697 CTGAGATTTGGAGCTCAGTCCAGGTCCTCCGCCACTGGATGGTGTCTGCTGTGGAAC 756  
QY 721 CTTGTAAACCAATGGGGTAACTGGGNAATCAATGAAGATTTCTGTGGGGTGGG 780  
Db |||||  
QY 757 CTTGTAAACCAATGGGGTAACTGGGNAATCAATGAAGATTTCTGTGGGGTGGG 816  
QY 781 GTGGGGAGTGTGGGAATCATTTCTGTAAATGGTAACCTGCAAGTGTACCCCTGAGCC 840  
Db |||||  
QY 817 GTGGGGAGTGTGGGNAATCATTTCTGTCTTAAATGGTAACTGCAAGTGTACCCCTGAGCC 876  
QY 841 CCGCAGGCCAACCCATCCCGAGTGTAGAGCTTTAGGGTCAATGAGTCTCCACATGAAGTC 900  
Db |||||  
QY 877 CCGCAGGCCAACCCATCCCGAGTGTAGAGCTTTAGGGTCAATGAGTCTCCACATGAAGTC 936  
QY 901 CTCTCACTCAACCTGTGACGAGAGAGGAGGTGTATAGAGTCAAGGATCTATGSCCT 960  
Db |||||  
QY 937 CTGTCACTCAACCTGTGACGAGAGAGGAGGTGTATAGAGTCAAGGATCTATGSCCT 996  
QY 961 TGGCCAGGCCCCCTTTCCCTTT-ATCCTGCCACTGTCAATGCTACCTTTCCCTATC 1019  
Db |||||  
QY 997 TGGCCAGGCCCCCTTTCCCTTTAACTCTGCCACTGTCAATGCTACCTTTCCCTATC 1056  
QY 1020 TCTTCCCTCATCATCTTTGTTGTGGGCATAGAGAGGTGGTGAATGTCAAGAAATGGTTGG 1079  
Db |||||  
QY 1057 TCTTCCCTCATCATCTTTGTTGTGGGCATAGAGAGGTGGTGAATGTCAAGAAATGGTTGG 1116  
QY 1080 AGCTCAGAAGATAAAGATAAGTAGGTATGCTGATCCTCTTTTAAACCCCAAGATACA 1139  
Db |||||  
QY 1117 AGCTCAGAAGATAAAGATAAGTAGGTATGCTGATCCTCTTTTAAACCCCAAGATACA 1176  
QY 1140 ATCAAAATCCAGATGCTGCTCTAATTCGCATGAAAGAGTGTCTCATGACATATTGAGAA 1199  
Db |||||  
QY 1177 ATCAAAATCCAGATGCTGCTCTAATTCGCATGAAAGAGTGTCTCATGACATATTGAGAA 1236  
QY 1200 GACCTACTTAAAGTGGCATATATTGCAATTTATTTAATTAAGATACCTATTATTA 1259  
Db |||||  
QY 1237 GACCTACTTAAAGTGGCATATATTGCAATTTATTTAATTAAGATACCTATTATTA 1296  
QY 1260 TATTTCTTATAGAAAAGTCTGGAAGAGTTTACTTCAATTTGAGCAATGTGAGGGTGG 1319  
Db |||||  
QY 1297 TATTTCTTTATAGAAAAGTCTGGAAGAGTTTACTTCAATTTGAGCAATGTGAGGGTGG 1356

QY 1320 TGGCAGTATAGGTGAATTTTCTTTAAATTCGTTAAATTTATCTGATTTCTCTAATTTTC 1379  
Db |||||  
QY 1357 TGGCAGTATAGGTGAATTTTCTTTAAATTCGTTAAATTTATCTGATTTCTCTAATTTTC 1416  
Db |||||  
QY 1380 TACAAATGAAGATGAATTCCTTGTATAAAAATAAGAAAGAAATTAATCTTGAGGTAAAGCA 1439  
Db |||||  
QY 1417 TACAAATGAAGATGAATTCCTTGTATAAAAATAAGAAAGAAATTAATCTTGAGGTAAAGCA 1476  
QY 1440 GAGCAGACATCATCTCTGATTTGTCTCAGCCTCCAAATTCCTCCAGAGTAAATTCAAATTTGA 1499  
Db |||||  
QY 1477 GAGCAGACATCATCTCTGATTTGTCTCAGCCTCCAAATTCCTCCAGAGTAAATTCAAATTTGA 1536  
QY 1500 ATCAGAGTCTCTGCTCTGCTGTTGTTGTAGTAGTATCAGGAAACAGATCTCAGCAAGC 1559  
Db |||||  
QY 1537 ATCAGAGTCTCTGCTCTGCTGTTGTTGTAGTAGTATCAGGAAACAGATCTCAGCAAGC 1596  
QY 1560 CACTCAGCAGAGGCTGCTGAGTTTGTGTGGTGGAAATCTCTGGGTAAAGAACTTAA 1619  
Db |||||  
QY 1597 CACTCAGCAGAGGCTGCTGAGTTTGTGTGGTGGAAATCTCTGGGTAAAGAACTTAA 1656  
QY 1620 GAAACAAAATCATCTGTTAAATTTCTTCTAGAAGATCAGAGCCCTGGGATTCAGAGC 1679  
Db |||||  
QY 1657 GAAACAAAATCATCTGTTAAATTTCTTCTAGAAGATCAGAGCCCTGGGATTCAGAGC 1716  
QY 1680 ATTGATCAGTCTCTAAGAGGCTGCTGTTGTTGAATTTGTGTCCTCCTCAATTTCA 1739  
Db |||||  
QY 1717 ATTGATCAGTCTCTAAGAGGCTGCTGTTGTTGAATTTGTGTCCTCCTCAATTTCA 1776  
QY 1740 CATCTCTCTGGAATCTCAGTCTGAGTTTATTTGGAGATAAGGTCTCTCAGATGTAG 1799  
Db |||||  
QY 1777 CATCTCTCTGGAATCTCAGTCTGAGTTTATTTGGAGATAAGGTCTCTCAGATGTAG 1836  
QY 1800 TTAGTTAAAGACAAAGTCTATGCTGGATGAAGGTAGACCTTAAATTTCAATATGATCTGTTTCC 1859  
Db |||||  
QY 1837 TTAGTTAAAGACAAAGTCTATGCTGGATGAAGGTAGACCTTAAATTTCAATATGATCTGTTTCC 1896  
QY 1860 TTGATTAAGAGCAGAGACACAGACAGAGGACCGGGGAGAGTATGTAAAGATG 1919  
Db |||||  
QY 1897 TTGATTAAGAGCAGAGACACAGAGCAGAGGACCGGGGAGAGTATGTAAAGATG 1956  
QY 1920 AAGCAGAGATCGGAGTTTTCAGCCACAAAGCTAAGAAACACCAAGGATTTGGCAACCA 1979  
Db |||||  
QY 1957 AAGCAGAGATCGGAGTTTTCAGCCACAAAGCTAAGAAACACCAAGGATTTGGCAACCA 2016  
QY 1980 TCAGAGCTTGAAGAGGCAAGAAATTTCTTCCCTAGAGGCTTTAGAGGATTAACGGC 2039  
Db |||||  
QY 2017 TCAGAGCTTGAAGAGGCAAGAAATTTCTTCCCTAGAGGCTTTAGAGGATTAACGGC 2076  
QY 2040 TCTGCTGAACCTTAAATCTCAGACTTCCAGCCTCTGAAACGAAAGAAATAAATTTTCGG 2099  
Db |||||  
QY 2077 TCTGCTGAACCTTAAATCTCAGACTTCCAGCCTCTGAAACGAAAGAAATAAATTTTCGG 2136  
QY 2100 CTGTTTAAAGCCACCAAGGATAATTTGGTTTACAGAGCTCTAGGAAACTAATACAGTGT 2159  
Db |||||  
QY 2137 CTGTTTAAAGCCACCAAGGATAATTTGGTTTACAGAGCTCTAGGAAACTAATACAGTGT 2196  
QY 2160 AAAATGATCCCTGTCTCTCTGTTTAAATTTCTGTTGTTCCCTCCACAAATGTACCA 2219  
Db |||||  
QY 2197 AAAATGATCCCTGTCTCTCTGTTTAAATTTCTGTTGTTCCCTCCACAAATGTACCA 2256  
QY 2220 AAGTTGCTTTTGTGACCCCAATAGAAATATGGCAGAGTATGTCATGCCACTTTCCAAGATT 2279  
Db |||||  
QY 2257 AAGTTGCTTTTGTGA-CCAATAGAAATATGGCAGAGTATGTCATGCCACTTTCCAAGATT 2315  
QY 2280 AGTTTAAAGACACTGACGCTTCTACTTGAAGCCCTCTCTCTGTCACCCACCGCCCC 2339  
Db |||||  
QY 2316 AGTTTAAAGACACTGACGCTTCTACTTGAAGCCCTCTCTCTGTCACCCACCGCCCC 2375  
QY 2340 CAATCTATCTTGGCTCACTCGCTCTGGGGAGAGTGTGCTGCTATGAGCAGGCTTA 2399  
Db |||||  
QY 2376 CAATCTATCTTGGCTCACTCGCTCTGGGGAGAGTGTGCTGCTATGAGCAGGCTTA 2435  
QY 2400 TAAAGAGACTTAGCTGTTAAATAATGAAGTCTCTCTGCCACAGCCACATTAGTGAACCTA 2459

Db 2436 TAAAGAGACTTACGTGGTAAATAATGAGTCTCTCCACACCCACATTAGTGAACCTA 2495  
Qy 2460 GAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTAAAGTTCCTCAGTTTGGTCT 2519  
Db 2496 GAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTAAAGTTCCTCAGTTTGGTCT 2555  
Qy 2520 AACTTGTATGACCAATAGATAAATAATATGACAGAAAGAG 2562  
Db 2556 AACTTGTATGACCAATAGATAAATAATATGACAGAAAGAG 2598

RESULT 5  
ID ABL95718 standard; cDNA; 2598 BP.  
XX ABL95718;  
AC ABL95718;  
DT 19-JUL-2002 (first entry)  
XX Human angiogenesis related cDNA PRO4342 SEQ ID NO: 315.  
DE Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
XX atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
KW cardiac; cytostatic; antiangiogenic; hypotensive; vulnery;  
KW antiarteriosclerotic; gene; ss.  
XX Homo sapiens.  
OS Homo sapiens.  
XX WO200208284-A2.  
XX 31-JAN-2002.  
XX 09-JUL-2001; 2001WO-US021735.  
PR 20-JUL-2000; 2000US-0219556P.  
PR 25-JUL-2000; 2000US-0220624P.  
PR 25-JUL-2000; 2000US-0220664P.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 02-AUG-2000; 2000US-0222695P.  
PR 17-AUG-2000; 2000US-00643657.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 07-SEP-2000; 2000US-0230978P.  
PR 18-SEP-2000; 2000US-00664610.  
PR 18-SEP-2000; 2000US-00665350.  
PR 24-OCT-2000; 2000US-0242922P.  
PR 08-NOV-2000; 2000US-00709238.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 22-JAN-2001; 2001US-00767609.  
PR 28-FEB-2001; 2001US-00796498.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 09-MAR-2001; 2001US-0080706.  
PR 14-MAR-2001; 2001US-00808689.  
PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 30-MAY-2001; 2001US-00870574.  
PR 30-MAY-2001; 2001WO-US017443.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
XX (GETH ) GENENTECH INC.  
PA (BAKE/) BAKER K P.

(FERR/) FERRARA N.  
(GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (MARS/) MARSTERS S A.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (STEP/) STEPHAN J F.  
PA (WATA/) WATANABE C K.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
XX  
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
XX  
DR WPI; 2002-171999/22.  
DR P-PSDB; ABB95580.  
XX  
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
PT infarction), endothelial or angiogenic disorders in a mammal.  
XX  
PS Claim 1; Fig 315; 567pp; English.  
XX  
CC The present invention provides the protein and coding sequences of human  
CC PRO proteins. These are useful for treating or diagnosing a  
CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
CC hypertrophy, trauma, cancer, age-related macular degeneration,  
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
CC healing. The present sequence is a coding sequence of the invention  
XX  
SQ Sequence 2598 BP; 687 A; 590 C; 648 G; 673 T; 0 U; 0 Other;  
Query Match 98.1%; Score 2514.2; DB 6; Length 2598;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 2552; Conservative 0; Mismatches 8; Indels 3; Gaps 3;  
Qy 1 AGGGAGTCTACACCTGTGGAGCTCAAGATGGTCTCTGAGTGGGGCGCTGTGTTCCGAA 60  
Db 38 AGGGAGTCTACACCTGTGGAGCTCAAGATGGTCTCTGAGTGGGGCGCTGTGTTCCGAA 97  
Qy 61 TGAAGACTCGGCATTTGAAGTGGTCTTATCTGCATATAACCACTTCTAGCTGGAGGC 120  
Db 98 TGAAGACTCGGCATTTGAAGTGGTCTTATCTGCATATAACCACTTCTAGCTGGAGGC 157  
Qy 121 TGCATGCGAGGAAGGTCAATTAAGGTGAAGAGATCAGCGTGGTCCCAATCGGTGGCTGG 180  
Db 158 TGCATGCGAGGAAGGTCAATTAAGGTGAAGAGATCAGCGTGGTCCCAATCGGTGGCTGG 217  
Qy 181 ATGCCAGCTGTCCCGCTCATCTGGGTGTCCAGGGTGAAGCCAGTGCCTGTCAATG 240  
Db 218 ATGCCAGCTGTCCCGCTCATCTGGGTGTCCAGGGTGAAGCCAGTGCCTGTCAATG 277  
Qy 241 GGGTGGGCGAGGCGGACTCTAACACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG 300  
Db 278 GGGTGGGCGAGGCGGACTCTAACACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG 337  
Qy 301 GTGCCAAGGAATCCCAAGAGCTTCACTTCTACGGGGGAGACATGGGGCTCACCTCCAGCT 360  
Db 338 GTGCCAAGGAATCCCAAGAGCTTCACTTCTACGGGGGAGACATGGGGCTCACCTCCAGCT 397  
Qy 361 TCGAGTCGGCTGCCTACCCGGGTGCTGCTGTGACCGGTGCTGAAGCCGATCAGCCTG 420  
Db 398 TCGAGTCGGCTGCCTACCCGGGTGCTGCTGTGACCGGTGCTGAAGCCGATCAGCCTG 457  
Qy 421 TCAGACTACCCAGCTTCCCGAGATGTGGGTGGATGCCCCCATCAACAGACTTCTACT 480

Db 458 TCAGACTACCCAGCTTCCCGAGATGGTGGCTGGAATGCCCCCATCAGACTTCTACT 517  
 Qy 481 TCAGCAGTGTGACTAGGGCAACGTGCCCCCCCAGAACTCCCTGGGAGAGCCAGCTCGG 540  
 Db 518 TCAGCAGTGTGACTAGGGCAACGTG - CCCCCAGAACTCCCTGGGAGAGCCAGCTCGG 576  
 Qy 541 GTGAGGGGTGAGTGGAGAGACCCATGGCGGACAACTCACTCTTCTGTCTCAGAACCCC 600  
 Db 577 GTGAGGGGTGAGTGGAGAGACCCATGGCGGACAACTCACTCTTCTGTCTCAGAACCCC 636  
 Qy 601 CAGGTCTGACTTAGTGGGACCTGACCACTTGTCTTCTGGTTCCTCAGTTTGCATAAATT 660  
 Db 637 CAGCTCTGACTTAGTGGGACCTGACCACTTGTCTTCTGGTTCCTCAGTTTGCATAAATT 696  
 Qy 661 CTGAGATTTGGAGCTCAGTCCAGGGTCTCCGCCACTGATGGTCTACTGTGTGGAAC 720  
 Db 697 CTGAGATTTGGAGCTCAGTCCAGGGTCTCCGCCACTGATGGTCTACTGTGTGGAAC 756  
 Qy 721 CTTGTAAACCATGTGGGTAACCTGGGAATAACATGAAGAAAGATTCTGTGGGGGTGG 780  
 Db 757 CTTGTAAACCATGTGGGTAACCTGGGAATAACATGAAGAAAGATTCTGTGGGGGTGG 816  
 Qy 781 GTGGGGAGTGTGGGAATCACTTCTGCTTAATGGTAACTGAAGTGTAACTCTGAGCC 840  
 Db 817 GTGGGGAGTGTGGGAATCACTTCTGCTTAATGGTAACTGAAGTGTAACTCTGAGCC 876  
 Qy 841 CCGAGGCCAACCCATCCCGAGTTGAGCCTTATAGGGTCAGTAGCTCTCCACATGAAGTC 900  
 Db 877 CCGAGGCCAACCCATCCCGAGTTGAGCCTTATAGGGTCAGTAGCTCTCCACATGAAGTC 936  
 Qy 901 CTCTCACTCACTGTCAGGAGAGAGGGTGGTCAATAGAGTCAGGGATCTATGGCCCT 960  
 Db 937 CTGTCACTCACTGTCAGGAGAGAGGGTGGTCAATAGAGTCAGGGATCTATGGCCCT 996  
 Qy 961 TGGCCAGCCGCCACCCCTTCCCTTT - ATCCGCACTGTGCATATGCTACCTTCTCTATC 1019  
 Db 997 TGGCCAGCCGCCACCCCTTCCCTTTAACTCCGCCACTGTCATATGCTACCTTCTCTATC 1056  
 Qy 1020 TCTTCCCTCATCATCTTGTGTGGCATAGAGAGTGGTATGTCAGAGAAATGGTTCG 1079  
 Db 1057 TCTTCCCTCATCATCTTGTGTGGCATAGAGAGTGGTATGTCAGAGAAATGGTTCG 1116  
 Qy 1080 AGCTCAGAAGATAAAGATAAGTAGGGTATGCTGATCCTCTTTTAAACCCCAAGATACA 1139  
 Db 1117 AGCTCAGAAGATAAAGATAAGTAGGGTATGCTGATCCTCTTTTAAACCCCAAGATACA 1176  
 Qy 1140 ATCAAAATCCAGATGCTGCTCTATTCCTAGTAAAGAGTCTCATGATATTCAGAA 1199  
 Db 1177 ATCAAAATCCAGATGCTGCTCTATTCCTAGTAAAGAGTCTCATGATATTCAGAA 1236  
 Qy 1200 GACCTACTTACAAAGTGGCATATATGCAATTTATTTAATTAAGATACCTATTATATA 1259  
 Db 1237 GACCTACTTACAAAGTGGCATATATGCAATTTATTTAATTAAGATACCTATTATATA 1296  
 Qy 1260 TATTTCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATGTGAGCAATGTGAGGGTGG 1319  
 Db 1297 TATTTCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATGTGAGCAATGTGAGGGTGG 1356  
 Qy 1320 TGGCAGTATAGGTGATTTTCTTTTAACTTCTGTTAAATTTATCTGATTTCTTAAATTTTC 1379  
 Db 1357 TGGCAGTATAGGTGATTTTCTTTTAACTTCTGTTAAATTTATCTGATTTCTTAAATTTTC 1416  
 Qy 1380 TACAATGAAGATGAATTCCTGTATTAATAAATAAGAAAGAAATTAATCTTGAGTAAAGCA 1439  
 Db 1417 TACAATGAAGATGAATTCCTGTATTAATAAATAAGAAAGAAATTAATCTTGAGTAAAGCA 1476  
 Qy 1440 GAGCAGACATCATCTCTGATTTGCTCTGAGCCTCCAAATTCCTCAGAGTAAATTCAAATTGA 1499  
 Db 1477 GAGCAGACATCATCTCTGATTTGCTCTCAGCCTCCCAATTCCTCAGAGTAAATTCAAATTGA 1536  
 Qy 1500 ATCGAGCTCTGCTGCTCTGTTGGTTGGTGTAGTAGTATCAGGAAAACAGATCTCAGCAAGC 1559  
 Db 1537 ATCGAGCTCTGCTGCTCTGTTGGTTGGTGTAGTAGTATCAGGAAAACAGATCTCAGCAAGC 1596

Qy 1560 CACTGAGGAGAGGCTGTGCTGAGTTTGTGTGCTGGAATCTCTGGGTAGGAACTTAAA 1619  
 Db 1597 CACTGAGGAGAGGCTGTGCTGAGTTTGTGTGCTGGAATCTCTGGGTAGGAACTTAAA 1656  
 Qy 1620 GAACAAAAATCATCTGTAATTTCTTCTAGAGGATACAGCCCTTGGGATTTCCAGGC 1679  
 Db 1657 GAACAAAAATCATCTGTAATTTCTTCTAGAGGATACAGCCCTTGGGATTTCCAGGC 1716  
 Qy 1680 ATTGGATCCAGTCTCTAAGAGGCTGTGCTGCTGGAATTTGTGTCCTCCCTCAAATTCA 1739  
 Db 1717 ATTGGATCCAGTCTCTAAGAGGCTGTGCTGCTGGAATTTGTGTCCTCCCTCAAATTCA 1776  
 Qy 1740 CATCTTCTTTGGAAATCTCAGTCTGTGATTTATTTGGAGATAAGTCTCTGCGAGATGAG 1799  
 Db 1777 CATCTTCTTTGGAAATCTCAGTCTGTGATTTATTTGGAGATAAGTCTCTGCGAGATGAG 1836  
 Qy 1800 TTAGTTAAGACAGGTCATGCTGATGAAGTGAAGTAAATTCATATATGACTGTTTCC 1859  
 Db 1837 TTAGTTAAGACAGGTCATGCTGATGAAGTGAAGTAAATTCATATATGACTGTTTCC 1896  
 Qy 1860 TTGTATGAAGAGGAGACACACAGACAGAGAGACGCGGGGAAGACTATGTAAAGATG 1919  
 Db 1897 TTGTATGAAGAGGAGACACACAGACAGAGAGAGACGCGGGGAAGACTATGTAAAGATG 1956  
 Qy 1920 AAGCAGAGATCGGAGTTTTCAGCCACAGCTAAGAAACACCAAGGATTTGTGCGCAACCA 1979  
 Db 1957 AAGCAGAGATCGGAGTTTTCAGCCACAGCTAAGAAACACCAAGGATTTGTGCGCAACCA 2016  
 Qy 1980 TCAGAGCTCTGGAAGAGCAAGAGAAATCTTCCCTAGAGCTTTAGAGGGATAAGCGC 2039  
 Db 2017 TCAGAGCTCTGGAAGAGCAAGAGAAATCTTCCCTAGAGCTTTAGAGGGATAAGCGC 2076  
 Qy 2040 TCTGTGAAACCTTAATCTCAGACTTCCAGCTCTGAAACGAAAGAAATTAATTTTCG 2099  
 Db 2077 TCTGTGAAACCTTAATCTCAGACTTCCAGCTCTGAAACGAAAGAAATTAATTTTCG 2136  
 Qy 2100 CTGTTTAAAGCCACCAAGATAATTTGGTTACAGAGCTCTAGGAACTTAATACAGCTGCT 2159  
 Db 2137 CTGTTTAAAGCCACCAAGATAATTTGGTTACAGAGCTCTAGGAACTTAATACAGCTGCT 2196  
 Qy 2160 AAAATGATCCCTGTCTCTCGTGTTTTACATTTCTGTGTGTCTCCCTCCCAATGTACCA 2219  
 Db 2197 AAAATGATCCCTGTCTCTCGTGTTTTACATTTCTGTGTGTCTCCCTCCCAATGTACCA 2256  
 Qy 2220 AAGTTGTCTTTGTACCCAAATAGAAATATGGCAGAGTATGGCATGGCATTCCAAAGATT 2279  
 Db 2257 AAGTTGTCTTTGTGA - CCAATAGAAATATGGCAGAGTATGGCATGGCATTCCAAAGATT 2315  
 Qy 2280 AGTTTAAAGACACTGCGCTTCTAGAGCTCTCTCTGAGCCCTCTCTCTGCGCCACCCGCCCCC 2339  
 Db 2316 AGTTTAAAGACACTGCGCTTCTAGAGCTCTCTCTGAGCCCTCTCTCTGCGCCACCCGCCCCC 2375  
 Qy 2340 CAATCTATCTTGGCTCACTCGCTCTGGGGAGCTAGCTGCGCATGTATGAGCAGGCTTA 2399  
 Db 2376 CAATCTATCTTGGCTCACTCGCTCTGGGGAGCTAGCTGCGCATGTATGAGCAGGCTTA 2435  
 Qy 2400 TAAAGAGATTAAGTGTGTAATAAATAAGTCTTCTGCGCCACAGCCACATTAAGTGAACCTTA 2459  
 Db 2436 TAAAGAGATTAAGTGTGTAATAAATAAGTCTTCTGCGCCACAGCCACATTAAGTGAACCTTA 2495  
 Qy 2460 GAAGCAGAGCTCTGTGAGATAATCGATGTTTGTGTTTAAAGTTGCTCAGTTTTTGGTCT 2519  
 Db 2496 GAAGCAGAGCTCTGTGAGATAATCGATGTTTGTGTTTAAAGTTGCTCAGTTTTTGGTCT 2555  
 Qy 2520 AACTGTTTATGCAAGCAATAGATAAATAATATGCAAGAAAGAG 2562  
 Db 2556 AACTGTTTATGCAAGCAATAGATAAATAATATGCAAGAAAGAG 2598

XX AC AKA1239;  
XX DT 11-JUL-2003 (first entry)  
XX DE Novel human secreted and transmembrane protein PRO4342 cDNA.  
XX DE Human; secreted and transmembrane protein; PRO; antibody therapy;  
KW pharmaceutical; diagnostic; biosensor; bioreactor; gene; ss.  
XX OS Homo sapiens.  
XX US2003018173-A1.  
XX PN 23-JAN-2003.  
XX PD 01-MAY-2002; 2002US-00063515.  
XX PF 06-DEC-2001; 2001US-00006867.  
XX PR (GETH ) GENENTECH INC.  
XX PA Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
XX PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
XX XX WPI; 2003-401702/38.  
DR P-PSDB; ABU90951.  
XX XX New antibody useful for identifying PRO polypeptides, for affinity  
PT purification of PRO polypeptides, and for preparing a medicament for  
PT diagnosing or treating conditions responsive to the antibody or PRO  
PT polypeptide.  
XX PS Disclosure; Fig 151; 345pp; English.  
XX CC The invention describes an antibody that specifically binds to a PRO  
CC polypeptide having a fully defined amino acid sequence given in the  
CC specification. The antibody is useful in identifying PRO polypeptides  
CC useful for various industrial applications, including pharmaceuticals,  
CC diagnostics, biosensors and bioreactors. The antibody is also used for  
CC affinity purification of PRO polypeptides from recombinant cell culture  
CC or natural sources. The antibody, PRO polypeptide, or its agonists or  
CC antagonists, may be used for preparing a medicament for diagnosing or  
CC treating a condition responsive to the antibody, PRO polypeptide, or its  
CC agonists or antagonists. This sequence encodes a novel human secreted and  
CC transmembrane PRO polypeptide  
XX SQ Sequence 2598 BP; 687 A; 590 C; 648 G; 673 T; 0 U; 0 Other;  
  
Query Match 98.1%; Score 2514.2; DB 8; Length 2598;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 2552; Conservative 0; Mismatches 8; Indels 3; Gaps 3;  
  
QY 1 AGGGAGTCTACACCTGTGGAGCTCAAGATGGTCTGAGTGGGGCGTGTCTCCGAA 60  
DB 38 AGGGAGTCTACACCTGTGGAGCTCAAGATGGTCTGAGTGGGGCGTGTCTCCGAA 97  
  
QY 61 TGAAGACTCGGCATTGAAGGTGCTTTATCTGCATAATAACAGCTTCTAGCTGGAGGC 120  
DB 98 TGAAGACTCGGCATTGAAGGTGCTTTATCTGCATANTAAACAGCTTCTAGCTGGAGGC 157  
  
QY 121 TGCATGCGGGAGGTGCTTTAAAGGTGAAGAGATCAGCGTGGTCCCAATCGGTGGCTGG 180  
DB 158 TGCATGCGGGAGGTGCTTTAAAGGTGAAGAGATCAGCGTGGTCCCAATCGGTGGCTGG 217  
  
QY 181 ATGCCAGCTGTCCTCCCGTCACTCGGTGTCCAGGTGGAAGCCAGTCCCTGTCTATGTG 240  
DB 218 ATGCCAGCTGTCCTCCCGTCACTCGGTGTCCAGGTGGAAGCCAGTCCCTGTCTATGTG 277  
  
QY 241 GGTGGGGCAGGAGCCGCTCTAACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG 300  
DB 278 GGTGGGGCAGGAGCCGCTCTAACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG 337

QY 301 GTGCCAAGGAATCCAAAGAGCTTCACTTCTACGGCGGACATGGGGCTCACCTCCAGCT 360  
DB 338 GTGCCAAGGAATCCAAAGAGCTTCACTTCTACGGCGGACATGGGGCTCACCTCCAGCT 397  
  
QY 361 TCGAGTCGGCTCGCTACCGGGCTGGTTCCTGTGCACGGTGGCTGAAGCCGATCAGCCTG 420  
DB 398 TCGAGTCGGCTCGCTACCGGGCTGGTTCCTGTGCACGGTGGCTGAAGCCGATCAGCCTG 457  
  
QY 421 TCAGACTACCCAGCTTCCCGAAGATGGTGGCTGGATGCCCCATCAGAGCTTCTACT 480  
DB 458 TCAGACTACCCAGCTTCCCGAAGATGGTGGCTGGATGCCCCATCAGAGCTTCTACT 517  
  
QY 481 TCCAGCAGTGTGACTAGGCAACGTCGCCCCCGAGAACTCCCTGGGAGAGCCAGCTCGG 540  
DB 518 TCCAGCAGTGTGACTAGGCAACGTCGCCCCCGAGAACTCCCTGGGAGAGCCAGCTCGG 576  
  
QY 541 GTGAGGGGTGAGTGGAGAGACCCATGGCGGACAACTCACTTCTCTGTCTCTCAGGACCCC 600  
DB 577 GTGAGGGGTGAGTGGAGAGACCCATGGCGGACAACTCACTTCTCTGTCTCTCAGGACCCC 636  
  
QY 601 CAGGTCTGACTTGTAGTGGGCACCTGACCACTTGTCTTCTGTGGTTCAGATTAATAAT 660  
DB 637 CACGTCTGACTTGTAGTGGGCACCTGACCACTTGTCTTCTGTGGTTCAGATTAATAAT 696  
  
QY 661 CTGAGATTTGGAGCTCAGTCCAGGGTCCCTCCCGACCTGGATGGTCTGCTGTGGAAC 720  
DB 697 CTGAGATTTGGAGCTCAGTCCAGGGTCCCTCCCGACCTGGATGGTCTGCTGTGGAAC 756  
  
QY 721 CTTGTAAAAACCATGTGGGGTAACTGGGAATAAATGAAAGATTTCTGTGGGGTGGG 780  
DB 757 CTTGTAAAAACCATGTGGGGTAACTGGGAATAAATGAAAGATTTCTGTGGGGTGGG 816  
  
QY 781 GTGGGGAGTGTCTGGGAATCATTCCTGTCTTAATGTGTAATGTAAGTGTACCTCGAGCC 840  
DB 817 GTGGGGAGTGTCTGGGAATCATTCCTGTCTTAATGTGTAATGTAAGTGTACCTCGAGCC 876  
  
QY 841 CCGCAGGCCAACCCATCCCACTTGGAGCTTATAGGTGAGTCTCTCCACATGAAGTC 900  
DB 877 CCGCAGGCCAACCCATCCCACTTGGAGCTTATAGGTGAGTCTCTCCACATGAAGTC 936  
  
QY 901 CTCTCACTCACCACCTGTGCAGGAGAGGGAGTGGTCTATAGAGTCAGGGATCTATGGCCCT 960  
DB 937 CTGTCACTCACCACCTGTGCAGGAGAGGGAGTGGTCTATAGAGTCAGGGATCTATGGCCCT 996  
  
QY 961 TGGCCCGAGCCCAACCCCTTCCCTTT-ATCTGCGCACTGTCTATGCTACCTTTCTATC 1019  
DB 997 TGGCCCGAGCCCAACCCCTTCCCTTTAATCTCTCCACTGTCTATGCTACCTTTCTATC 1056  
  
QY 1020 TCTTCCCTCATCTCTTGTGTGGGCATGAGAGGTGGTGTGTCAGAGAAGATGGTTCG 1079  
DB 1057 TCTTCCCTCATCTCTTGTGTGGGCATGAGAGGTGGTGTGTCAGAGAAGATGGTTCG 1116  
  
QY 1080 AGCTCAGAAGATAAAGATAAGTGTAGGTATGCTGATCTCTTTTAAAAACCCAGATACA 1139  
DB 1117 AGCTCAGAAGATAAAGATAAGTGTAGGTATGCTGATCTCTTTTAAAAACCCAGATACA 1176  
  
QY 1140 ATCAAAATCCAGATGCTGCTCTATTTCCCATGAAAAAGTGTCTATGATATTCAGAA 1199  
DB 1177 ATCAAAATCCAGATGCTGCTCTATTTCCCATGAAAAAGTGTCTATGATATTCAGAA 1236  
  
QY 1200 GACCTACTTACAAAGTGGCATATATTGCAATTTTAAATTTAAAGATACCTATTATA 1259  
DB 1237 GACCTACTTACAAAGTGGCATATATTGCAATTTTAAATTTAAAGATACCTATTATA 1296  
  
QY 1260 TATTTCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTTGTAGCAATGTCAGGGTGG 1319  
DB 1297 TATTTCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTTGTAGCAATGTCAGGGTGG 1356  
  
QY 1320 TGGCAGTATAGTGTGATTTTTTTTAAATTTCTGTAAATTTATCTGTATTTCTTAATTTTC 1379  
DB 1357 TGGCAGTATAGTGTGATTTTTTTTAAATTTCTGTAAATTTATCTGTATTTCTTAATTTTC 1416  
  
QY 1380 TACAATGAAGATGAATTCCTTGTATAAAAATAAGAAAAATAATTAATCTTGTAGGTAAAGCA 1439





XX New isolated antibody specifically binding a PRO polypeptide, useful for  
PT the preparation of a medicament for treating disorders with the aberrant  
PT expression or activity of the PRO polypeptide, such as tumor conditions  
PT and cancer.  
XX  
PS Disclosure; Fig 151; 223pp; English.  
XX

CC The invention relates to an antibody that binds to a secreted or  
CC transmembrane protein designated PRO146 appearing as ABO33941. The  
CC protein is one of 84 PRO polypeptides which (along with their encoding  
CC nucleic acids) are disclosed in the specification. The methods and  
CC compositions of the present invention are useful for the preparation of a  
CC medicament for the treatment of disorders associated with the aberrant  
CC expression or activity of the PRO polypeptide, such as tumour conditions  
CC and cancer. They can also be used to generate transgenic or knockout  
CC animals useful in the development and screening of therapeutically useful  
CC reagents. The PRO polypeptides and encoding nucleic acids can be used as  
CC molecular weight markers for protein electrophoresis, chromosome  
CC identification and tissue typing. The antibodies may be used in various  
CC diagnostic, competitive binding and/or immunoprecipitation assays. The  
CC present sequence encodes a PRO polypeptide  
XX

SQ Sequence 2598 BP; 687 A; 590 C; 648 G; 673 T; 0 U; 0 Other;

Query Match 98.1%; Score 2514.2; DB 8; Length 2598;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 2552; Conservative 0; Mismatches 8; Indels 3; Gaps 3;

QY	1	AGGGAGCTACACCTGTGGAGCTCAAGATGGTCTGAGTGGGGCGCTGCTCCGAA	60
DB	38	AGGGAGCTACACCTGTGGAGCTCAAGATGGTCTGAGTGGGGCGCTGCTCCGAA	97
QY	61	TGAAGAGCTCGGCNTTGAAGGTGCTTTATCTGCAATAAACACAGCTTCTAGCTGGAGGC	120
DB	98	TGAAGAGCTCGGCNTTGAAGGTGCTTTATCTGCAATAAACACAGCTTCTAGCTGGAGGC	157
QY	121	TGCATGCGGGAAGGTCAATTAAGGTGAAGAGATCAGCGTGTGCCAATCGGTGGCTGG	180
DB	158	TGCATGCGGGAAGGTCAATTAAGGTGAAGAGATCAGCGTGTGCCAATCGGTGGCTGG	217
QY	181	ATGCCAGCTGTCCTCCGCTCATCTGGGTGTCAGGTGGAGCCAGTCCCTGTCATGTG	240
DB	218	ATGCCAGCTGTCCTCCGCTCATCTGGGTGTCAGGTGGAGCCAGTCCCTGTCATGTG	277
QY	241	GGGTGGGCGAGAGCCGACTCTAACTAGAGCCAGTGAACATCATGAGCTCTATCTTG	300
DB	278	GGGTGGGCGAGAGCCGACTCTAACTAGAGCCAGTGAACATCATGAGCTCTATCTTG	337
QY	301	GTGCCAAGGAATCCAAAGAGCTTCACTTCTACCGCGGAGCATGGGGCTCACTCCAGCT	360
DB	338	GTGCCAAGGAATCCAAAGAGCTTCACTTCTACCGCGGAGCATGGGGCTCACTCCAGCT	397
QY	361	TGAGTGGCGTGTCTACCGGGGTGTTCTGTGACGGTGTGCTGAAGCGGATCAGCCTG	420
DB	398	TGAGTGGCGTGTCTACCGGGGTGTTCTGTGACGGTGTGCTGAAGCGGATCAGCCTG	457
QY	421	TCAGACTCACCCAGCTTCCGGAATGGTGGGAATGCCCATCAAGACTTCTACT	480
DB	458	TCAGACTCACCCAGCTTCCGGAATGGTGGGAATGCCCATCAAGACTTCTACT	517
QY	481	TCCAGCAGTGTGACTAGGGCAAGCTGCCCGCCCGAGAACTCCCTGGGCGAGCCAGCTCG	540
DB	518	TCCAGCAGTGTGACTAGGGCAAGCTGCCCGCCCGAGAACTCCCTGGGCGAGCCAGCTCG	576
QY	541	GTGAGGGGTGAGTGGAGGAGACCCATGGCGGACAATCACTCTTCTGCTCTAGGACCCC	600
DB	577	GTGAGGGGTGAGTGGAGGAGACCCATGGCGGACAATCACTCTCTGCTCTAGGACCCC	636
QY	601	CAGGCTCTGAGTGGGACCTGACCACTTCTTCTGTTTCCAGTTTGCATAAAT	660
DB	637	CAGGCTCTGAGTGGGACCTGACCACTTCTTCTGTTTCCAGTTTGCATAAAT	696

QY	661	CTGAGATTTGGAGCTCAGTCCAGGGTCTCTCCCACTGGATGGTCTACTGCTGTGAAC	720
DB	697	CTGAGATTTGGAGCTCAGTCCAGGGTCTCTCCCACTGGATGGTCTACTGCTGTGAAC	756
QY	721	CTTTGAAAAACCATGTGGGGTAAACTGGGAATAAATGAAAGATTTCTGTGGGGTGGG	780
DB	757	CTTTGAAAAACCATGTGGGGTAAACTGGGAATAAATGAAAGATTTCTGTGGGGTGGG	816
QY	781	GTGGGGAGTGTGGGAATCATCTCTGCTTAATGTTAATGTAATGTAATGTAATGTAATG	840
DB	817	GTGGGGAGTGTGGGAATCATCTCTGCTTAATGTTAATGTAATGTAATGTAATGTAATG	876
QY	841	CGCGAGGCAACCCCATCCCACTGAGCCTTATAGGTCAGTGTCTCCACATGAAGTC	900
DB	877	CGCGAGGCAACCCCATCCCACTGAGCCTTATAGGTCAGTGTCTCCACATGAAGTC	936
QY	901	CTCTCACTCACCACCTGTGCAGGAGGAGGTGGTGCATAGAGTCAGGGATCTATGGCCCT	960
DB	937	CTGTCACTCACCACCTGTGCAGGAGGAGGTGGTGCATAGAGTCAGGGATCTATGGCCCT	996
QY	961	TGGCCAGCCCCACCCCTTCCCTTT-ATCCTGCCACTGTCTCATATGCTACCTTTCTTATC	1019
DB	997	TGGCCAGCCCCACCCCTTCCCTTTAAATCTCTGCCACTGTCTCATATGCTACCTTTCTTATC	1056
QY	1020	TCTTCCCTCATCATCTTGTGTGGGCATGAGGAGGTGGTGCATGTCAGAGAATGTTGG	1079
DB	1057	TCTTCCCTCATCATCTTGTGTGGGCATGAGGAGGTGGTGCATGTCAGAGAATGTTGG	1116
QY	1080	AGCTCAGAAGATAAAGATAGGTAGGGTATGCTGATCTCTTTTAAAAACCCCAAGATACA	1139
DB	1117	AGCTCAGAAGATAAAGATAGGTAGGGTATGCTGATCTCTTTTAAAAACCCCAAGATACA	1176
QY	1140	ATCAAAATCCAGATGCTGGTCTCTATTCCCATGAAAAAGTGTCTCATGATATGAGAA	1199
DB	1177	ATCAAAATCCAGATGCTGGTCTCTATTCCCATGAAAAAGTGTCTCATGATATGAGAA	1236
QY	1200	GACCTACTTACAAAGTGGCATATATGCAATTTATTTTAAATTAAGAGATACCTATTATA	1259
DB	1237	GACCTACTTACAAAGTGGCATATATGCAATTTATTTTAAATTAAGAGATACCTATTATA	1296
QY	1260	TATTTCTTTATAGAAAAAGTCTGGAAGAGTTTACTTTCAATTTGTAGCAATGTGAGGTGG	1319
DB	1297	TATTTCTTTATAGAAAAAGTCTGGAAGAGTTTACTTTCAATTTGTAGCAATGTGAGGTGG	1356
QY	1320	TGGCAGTATAGGTGATTTTCTTTTAAATTTCTGTATTTATCTGTATTTCTTAAATTTTC	1379
DB	1357	TGGCAGTATAGGTGATTTTCTTTTAAATTTCTGTATTTATCTGTATTTCTTAAATTTTC	1416
QY	1380	TACATGAAGATGAATTCCTTGTATATAAATAAGAAAAAGAAATTAATCTTGAGGTAGCA	1439
DB	1417	TACATGAAGATGAATTCCTTGTATATAAATAAGAAAAAGAAATTAATCTTGAGGTAGCA	1476
QY	1440	GAGCAGACATCATCTGATTTCTTCCAGCTCCCAATCCCGAGAGTAAATTCAAATTTGA	1499
DB	1477	GAGCAGACATCATCTGATTTCTTCCAGCTCCCAATCCCGAGAGTAAATTCAAATTTGA	1536
QY	1500	ATCGAGCTCTGCTGCTCTGGTTGGTTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG	1559
DB	1537	ATCGAGCTCTGCTGCTCTGGTTGGTTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG	1596
QY	1560	CACTGAGGAGGCTGTGCTGAGTTTGTGGCTGGAATCTCTGGGTGAAGAACTTAA	1619
DB	1597	CACTGAGGAGGCTGTGCTGAGTTTGTGGCTGGAATCTCTGGGTGAAGAACTTAA	1656
QY	1620	GAACAAAATCATCTGGTAAATTTCTTCTAGAGGATCACAGCCCTGGGATTTCCAGGC	1679
DB	1657	GAACAAAATCATCTGGTAAATTTCTTCTAGAGGATCACAGCCCTGGGATTTCCAGGC	1716
QY	1680	ATTGGATCCAGTCTCTAAGAAGGCTGCTGATCTGTTGTAATTTGTCTCCCTCAATTTCA	1739
DB	1717	ATTGGATCCAGTCTCTAAGAAGGCTGCTGATCTGTTGTAATTTGTCTCCCTCAATTTCA	1776
QY	1740	CATCCTTCTTGGAAATCTCAGTCTGTGAGTTTATTTGGAGATAAGGTCTCTGCGAGATGTAG	1799



Db 1777 CATCTCTTGGAACTCTAGTCTGAGTTTATTTGGAGATAAGTCTCTGCAGATGAG 1836  
Qy 1800 TTAGTTAAGACAAGGTCATGCTGGATGAAGGTAGACCTTAAATTCATATGACTGTTTCC 1859  
Db 1837 TTAGTTAAGACAAGGTCATGCTGGATGAAGGTAGACCTTAAATTCATATGACTGTTTCC 1896  
Qy 1860 TTCTATGAAGAGGAGGACACAGACAGAGAGAGAGCGGGGAAAGACTATGTAAGATG 1919  
Db 1897 TTGTATGAAGAGGAGGACACAGACAGAGAGAGAGCGGGGAAAGACTATGTAAGATG 1956  
Qy 1920 AAGGCAGAGATCGGAGTTTTGTCAGCCACCAAGCTAAGAAACACCAAGGATTTGGCAACCA 1979  
Db 1957 AAGGCAGAGATCGGAGTTTTGTCAGCCACCAAGCTAAGAAACACCAAGGATTTGGCAACCA 2016  
Qy 1980 TCAGAGCTTTGAAGAGGCAAGAGAAATTCCTCTAGAGGCTTTAGAGGATTAACGGC 2039  
Db 2017 TCAGAGCTTTGAAGAGGCAAGAGAAATTCCTCTAGAGGCTTTAGAGGATTAACGGC 2076  
Qy 2040 TCTGCTGAACCTTAAATCTCAGACTTCCAGCTCTCCTGAACGAAGAAATAAATTTGG 2099  
Db 2077 TCTGCTGAACCTTAAATCTCAGACTTCCAGCTCTCCTGAACGAAGAAATAAATTTGG 2136  
Qy 2100 CTGTTTTAAGCCACCAAGGATAATTTGGTTACAGCAGCTCTAGGAACTAATACAGTGT 2159  
Db 2137 CTGTTTTAAGCCACCAAGGATAATTTGGTTACAGCAGCTCTAGGAACTAATACAGTGT 2196  
Qy 2160 AATATGATCCCTGCTCTCTGCTGTTTACATTTGTTGTTGTCCTCCACCAATGACCA 2219  
Db 2197 AATATGATCCCTGCTCTCTGCTGTTTACATTTGTTGTTGTCCTCCACCAATGACCA 2256  
Qy 2220 AAGTGTCTTTGACCCATAAGATATGCGAAGTGTGTCATGCGCACTTCCAGATT 2279  
Db 2257 AAGTGTCTTTGAC-CCATAGAAATATGCGAAGTGTGTCATGCGCACTTCCAGATT 2315  
Qy 2280 AAGTTATAAAGACACTGACGCTTTACTTTGAGCCCTCTCTCTGTCGCCACCAACGCCCC 2339  
Db 2316 AAGTTATAAAGACACTGACGCTTTACTTTGAGCCCTCTCTCTGTCGCCACCAACGCCCC 2375  
Qy 2340 CAATCTATCTTGGCTCACTGCTCTGGGGAAGCTAGTGCCTATGAGAGGCGCTA 2399  
Db 2376 CAATCTATCTTGGCTCACTGCTCTGGGGAAGCTAGTGCCTATGAGAGGCGCTA 2435  
Qy 2400 TAAAGAGACTTAGTGTGTAAAAATGAAGTCTCTCTGTCGCCACCAACGCGCTA 2459  
Db 2436 TAAAGAGACTTAGTGTGTAAAAATGAAGTCTCTCTGTCGCCACCAACGCGCTA 2495  
Qy 2460 GAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTAAAGTTCAGTTCAGTTCCT 2519  
Db 2496 GAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTAAAGTTCAGTTCAGTTCCT 2555  
Qy 2520 AACTGTTATGCGCAATAGATAAATAATATGAGAGAAAGAG 2562  
Db 2556 AACTGTTATGCGCAATAGATAAATAATATGAGAGAAAGAG 2598

RESULT 8

ACA60438 standard; cdna; 2598 BP.

XX AC ACA60438;

DT 11-JUN-2003 (first entry)

DE Novel human secreted and transmembrane protein PRO4342 cdna.

XX Human; secreted and transmembrane polypeptide; gene;  
KW ss. chromosome mapping; gene mapping; transgenic animal; knockout animal;  
KW therapeutic agent screening; chromosome identification; tissue typing;  
KW gene therapy.

XX Homo sapiens.

XX

PN US2003018183-A1.  
PD 23-JAN-2003.  
XX 01-MAY-2002; 2002US-00063512.  
PF 06-DEC-2001; 2001US-00006867.  
XX (GETH ) GENENTECH INC.  
PA Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PU;  
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
XX WPI; 2003-330984/31.  
DR P-PSDB; ABU72027.  
XX New secreted and transmembrane PRO polypeptides and nucleic acid  
PT molecules encoding the polypeptides, useful in gene therapy or preparing  
PT a medicament for treating a condition that is responsive to the PRO  
PT polypeptide or antibody.  
XX Disclosure; Fig 151; 409pp; English.  
XX The invention describes novel isolated PRO polypeptides. The PRO  
CC polypeptides or anti-PRO antibodies are useful in preparing a medicament  
CC for treating a condition that is responsive to the PRO polypeptide or  
CC antibody. The PRO nucleotide sequences may be used as hybridisation  
CC probes in chromosome and gene mapping, or in generating antisense RNA and  
CC DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in  
CC assays to identify other proteins or molecules involved in binding  
CC reaction, to generate transgenic animals or knockout animals, which in  
CC turn are useful in the development and screening of therapeutically  
CC useful reagents, for chromosome identification, and tissue typing. The  
CC PRO polypeptides and nucleic acid molecules are also useful in gene  
CC therapy, and as molecular weight markers for protein electrophoresis  
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for  
CC PRO, or for the affinity purification of PRO from recombinant cell  
CC culture or natural sources. This sequence encodes a novel human secreted  
CC and transmembrane PRO polypeptide

XX Sequence 2598 BP; 687 A; 590 C; 648 G; 673 T; 0 U; 0 Other;

Query Match 98.1%; Score 2514.2; DB 8; Length 2598;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 2552; Conservative 0; Mismatches 8; Indels 3; Gaps 3;

Qy 1 AGGGGAGTCTACACCTCTGGAGCTCAAGATGGTCTCAGTGGGCGCTGTGCTTCCGAA 60

Db 38 AGGGGAGTCTACACCTCTGGAGCTCAAGATGGTCTCAGTGGGCGCTGTGCTTCCGAA 97

Qy 61 TGAAGACTCGGCATTGAAGTGTCTTATCTGCATAATAACCAAGCTTCTAGCTGAGGCG 120

Db 98 TGAAGACTCGGCATTGAAGTGTCTTATCTGCATAATAACCAAGCTTCTAGCTGAGGCG 157

Qy 121 TGCATCGAGGAGTCTTAAAGTGAAGATCAGCGTGTGCCCAATCGTGGCTGG 180

Db 158 TGCATCGAGGAGGAGTCTTAAAGTGAAGATCAGCGTGTGCCCAATCGTGGCTGG 217

Qy 181 ATGCCAGCCTGTCCCCCGTCACTCTCGGTGTCCAGGTGGAAGCCAGTGCCTGTATG 240

Db 218 ATGCCAGCCTGTCCCCCGTCACTCTCGGTGTCCAGGTGGAAGCCAGTGCCTGTATG 277

Qy 241 GGGTGGGCGAGGCGGACTCTAACTAGACCCAGTGAACATCATGGAGCTCTATCTTG 300

Db 278 GGGTGGGCGAGGCGGACTCTAACTAGACCCAGTGAACATCATGGAGCTCTATCTTG 337

Qy 301 GTGCCAAGAAATCCAAAGAGCTTCACTTCTACCGCGGACATGGGCTTCACTCCAGCT 360

Db 338 GTGCCAAGAAATCCAAAGAGCTTCACTTCTACCGCGGACATGGGCTTCACTCCAGCT 397

Qy 361 TCGAGTTCGGCTGCCTACCCGGGCTGGTCTCTGTGCAAGGTCGCTGAAGCCGATCAGCCTG 420

Db 398 TCGAGTTCGGCTGCCTACCCGGGCTGGTCTCTGTGCAAGGTCGCTGAAGCCGATCAGCCTG 457

QY	421	TCAGACTACCCAGCTTCCCGAGAAATGGTGGCTGGAAATGCCCCCATCA	CAGACTTCTACT	480
DB	458	TCAGACTACCCAGCTTCCCGAGAAATGGTGGCTGGAAATGCCCCCATCA	CAGACTTCTACT	517
QY	481	TCAGCAGTGTCACTAGGCAACAGTGCCTCCCGAGAACTCCCTGGGCA	GAGCCAGCTCGG	540
DB	518	TCAGCAGTGTCACTAGGCAACAGTGCCTCCCGAGAACTCCCTGGGCA	GAGCCAGCTCGG	576
QY	541	GTGAGGGGTGAGTGGAGAGACCCATGGCGGCAATCACTCTTTCTGCT	CTCAGACCCC	600
DB	577	GTGAGGGGTGAGTGGAGAGACCCATGGCGGCAATCACTCTTTCTGCT	CTCAGACCCC	636
QY	601	CAGGTCTGACTTAGTGGGCACTGACCACTTTGTCTTTCTGGTTCACG	ATTTGCAATAAT	660
DB	637	CACGTCTGACTTAGTGGGCACTGACCACTTTGTCTTTCTGGTTCACG	ATTTGCAATAAT	696
QY	661	CTGAGATTGGAGCTCAGTCCAGGTCCTCCCGAGAACTCCCTGGTGG	AACT	720
DB	697	CTGAGATTGGAGCTCAGTCCAGGTCCTCCCGAGAACTCCCTGGTGG	AACT	756
QY	721	CTTTGAAAAACCATGTGGGCTAAACTGGGAATAACATGAAAAAGATT	CTGTGGGGTGGG	780
DB	757	CTTTGAAAAACCATGTGGGCTAAACTGGGAATAACATGAAAAAGATT	CTGTGGGGTGGG	816
QY	781	GTGGGGAGTGTGGGAATCATCTCTGCTTAATGGTAACTGACAAAGT	TTTACCTGAGCC	840
DB	817	GTGGGGAGTGTGGGAATCATCTCTGCTTAATGGTAACTGACAAAGT	TTTACCTGAGCC	876
QY	841	CCGCGAGCAACCCATCCCGAGTGGAGCTTATAGGTCAGTAGCTCTCC	ACATGAGTC	900
DB	877	CCGCGAGCAACCCATCCCGAGTGGAGCTTATAGGTCAGTAGCTCTCC	ACATGAGTC	936
QY	901	CTCTCACTCACCACCTGTGAGAGAGGAGTGGTCATAGAGTCAGGGAT	CTATGGCCCT	960
DB	937	CTGTCACTCACCACCTGTGAGAGAGGAGTGGTCATAGAGTCAGGGAT	CTATGGCCCT	996
QY	961	TGGCCAGCCCCACCCCTTCCCTTTT-ATCTGCCACTGTCTATGCTAC	CTTCTCTATC	1019
DB	997	TGGCCAGCCCCACCCCTTCCCTTTT-ATCTGCCACTGTCTATGCTAC	CTTCTCTATC	1056
QY	1020	TCTTCCCTCATCATCTTGTGTGGCAGTGGAGGCTGGTGTGATGATG	ATGAGTGGTGG	1079
DB	1057	TCTTCCCTCATCATCTTGTGTGGCAGTGGAGGCTGGTGTGATGATG	ATGAGTGGTGG	1116
QY	1080	AGCTCAGAAATAAAGATAGTGGGTATGCTGATCTCTTTTAAAAACC	CAAGATACA	1139
DB	1117	AGCTCAGAAATAAAGATAGTGGGTATGCTGATCTCTTTTAAAAACC	CAAGATACA	1176
QY	1140	ATCAAAATCCAGATGCTGCTCTATTTCCCATGAAAAAGTGTCTATG	ACATATTGAGAA	1199
DB	1177	ATCAAAATCCAGATGCTGCTCTATTTCCCATGAAAAAGTGTCTATG	ACATATTGAGAA	1236
QY	1200	GACCTACTTACAAAGTGGCATATATGCAATTTATTTTAAAGATAC	CTATTTATA	1259
DB	1237	GACCTACTTACAAAGTGGCATATATGCAATTTATTTTAAAGATAC	CTATTTATA	1296
QY	1260	TATTTCTTTATAGAAAAAGTCTGGAAGAGTTTACTTTCAATTTGT	AGCAATGTGAGGTCG	1319
DB	1297	TATTTCTTTATAGAAAAAGTCTGGAAGAGTTTACTTTCAATTTGT	AGCAATGTGAGGTCG	1356
QY	1320	TGGCAGTATAGGTGATTTTCTTTTAAATTTCTGTTAATTTTATCT	GTTATTTCTTAAATTTTC	1379
DB	1357	TGGCAGTATAGGTGATTTTCTTTTAAATTTCTGTTAATTTTATCT	GTTATTTCTTAAATTTTC	1416
QY	1380	TACATGAAAGTGAATTCCTGTATATAAAATAAGAAAAAGAAATTA	ATCTTGGAGTGAAGCA	1439
DB	1417	TACATGAAAGTGAATTCCTGTATATAAAATAAGAAAAAGAAATTA	ATCTTGGAGTGAAGCA	1476
QY	1440	GAGCAGACATCATCTGATCTGCTCCAGCTCCCAATCCCGAGTAA	ATTCAAATGCA	1499
DB	1477	GAGCAGACATCATCTGATCTGCTCCAGCTCCCAATCCCGAGTAA	ATTCAAATGCA	1536

QY	1500	ATCGAGCTCTGCTCTGCTTGGTTGTAGTATGATCAGGAAACAGATCT	CAGCAAGC	1559
DB	1537	ATCGAGCTCTGCTCTGCTTGGTTGTAGTATGATCAGGAAACAGATCT	CAGCAAGC	1596
QY	1560	CACGAGGAGGAGGCTGTCTGAGTTTGTGTGGCTGGAATCTCTGGGT	TAAGAACTTAAA	1619
DB	1597	CACGAGGAGGAGGCTGTCTGAGTTTGTGTGGCTGGAATCTCTGGGT	TAAGAACTTAAA	1656
QY	1620	GAACAAAAATCATCTGGTAAATTTCTTCTAGAAAGATCAACGCCCT	CTGGATTTCAAAGGC	1679
DB	1657	GAACAAAAATCATCTGGTAAATTTCTTCTAGAAAGATCAACGCCCT	CTGGATTTCAAAGGC	1716
QY	1680	ATTGATCCAGCTCTTAAGAAAGGCTGTCTAGTGGTGAATTTGTGTC	CCCTCAAAATTC	1739
DB	1717	ATTGATCCAGCTCTTAAGAAAGGCTGTCTAGTGGTGAATTTGTGTC	CCCTCAAAATTC	1776
QY	1740	CATCTCTTCTGGAATCTCAGTCTGTGAGTTTATTTGGAGATAAGGT	CTCTGCAGATGTAG	1799
DB	1777	CATCTCTTCTGGAATCTCAGTCTGTGAGTTTATTTGGAGATAAGGT	CTCTGCAGATGTAG	1836
QY	1800	TTAGTTAAAGACAAGGTCATGTGGATGAAGGTAGACCTTAAATTTCA	TATATGACTGTTTCC	1859
DB	1837	TTAGTTAAAGACAAGGTCATGTGGATGAAGGTAGACCTTAAATTTCA	TATATGACTGTTTCC	1896
QY	1860	TTGTATGAAAAAGAGAGGACACAGAGACAGAGAGACGCGGGAGACT	TATGTAAAGATG	1919
DB	1897	TTGTATGAAAAAGAGAGGACACAGAGACAGAGAGACGCGGGAGACT	TATGTAAAGATG	1956
QY	1920	AAGGACAGATCGGAGTTTTCAGCCACCAAGCTTAAGAAACCAAGAT	TTGTGCAACCA	1979
DB	1957	AAGGACAGATCGGAGTTTTCAGCCACCAAGCTTAAGAAACCAAGAT	TTGTGCAACCA	2016
QY	1980	TCAGAAGCTTGAAGAGGCAAGAAATTTCTTCCCTAGAGGCTTTT	PAGAGGATAACGCG	2039
DB	2017	TCAGAAGCTTGAAGAGGCAAGAAATTTCTTCCCTAGAGGCTTTT	PAGAGGATAACGCG	2076
QY	2040	TCTGCTGAAACCTTAAATCTCAGACTTCAGCCCTCTGAAGCAAGAA	ATAATTAATTTCCG	2099
DB	2077	TCTGCTGAAACCTTAAATCTCAGACTTCAGCCCTCTGAAGCAAGAA	ATAATTAATTTCCG	2136
QY	2100	CTGTTTTTAAGCCACCAAGGATAATTTGGTTACAGAGCTCTTAG	AAACTAATACAGCTGCT	2159
DB	2137	CTGTTTTTAAGCCACCAAGGATAATTTGGTTACAGAGCTCTTAG	AAACTAATACAGCTGCT	2196
QY	2160	AAAAATGATCCCTGCTCTCTGTTTACATTTCTGTGTGTCTCCCT	CCCAATGTACCA	2219
DB	2197	AAAAATGATCCCTGCTCTCTGTTTACATTTCTGTGTGTCTCCCT	CCCAATGTACCA	2256
QY	2220	AAGTTGTCTTTGTGACCAATAGATAATGGCAGAAAGTATGGCAT	GCCACTTCCAAAGTT	2279
DB	2257	AAGTTGTCTTTGTGACCAATAGATAATGGCAGAAAGTATGGCAT	GCCACTTCCAAAGTT	2315
QY	2280	AGTTTATAAAGACACTGCAGCTTCTACTTGGAGCCCTCTCTCTG	CCCAACCCGCCCC	2339
DB	2316	AGTTTATAAAGACACTGCAGCTTCTACTTGGAGCCCTCTCTCTG	CCCAACCCGCCCC	2375
QY	2340	CAATCTATCTTGGCTCACTCGCTCTGGGGAAAGTAGCTGCCAT	GTCTATGAGCAGCCCTA	2399
DB	2376	CAATCTATCTTGGCTCACTCGCTCTGGGGAAAGTAGCTGCCAT	GTCTATGAGCAGCCCTA	2435
QY	2400	TAAAGAGACTTACGTGGTAAAAAATGAAGTCTCTGCCCCACAGCC	CACTTAGTGAACCTA	2459
DB	2436	TAAAGAGACTTACGTGGTAAAAAATGAAGTCTCTGCCCCACAGCC	CACTTAGTGAACCTA	2495
QY	2460	GAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTAAAGT	CTCAGTTTTGCTCT	2519
DB	2496	GAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTAAAGT	CTCAGTTTTGCTCT	2555
QY	2520	AACCTGTTTATGAGCAATAGATAAATAATATGAGAGAAAGAG	2562	
DB	2556	AACCTGTTTATGAGCAATAGATAAATAATATGAGAGAAAGAG	2598	

RESULT 9
ACA58885
ID ACA58885 standard; cDNA; 2598 BP.
XX
XX
ACA58885;
XX
XX
DT
10-JUN-2003 (first entry)
XX
XX
cDNA encoding human secreted polypeptide
DE PRO4342

CC	The invention relates to an antibody that binds to a polypeptide with a
CC	fully defined sequence given in the specification. The methods and
CC	compositions (containing antibodies that specifically bind a PRO
CC	polypeptide) of the present invention are useful for the preparation of a
CC	medicament for the treatment of disorders associated with the aberrant
CC	expression or activity of the PRO polypeptide, such as tumour conditions
CC	and cancer. They can also be used to generate transgenic or knockout
CC	animals useful in the development and screening of therapeutically useful
CC	reagents. The PRO polypeptides and encoding nucleic acids can be used as
CC	molecular weight markers for protein electrophoresis, chromosome
CC	identification and tissue typing. The PRO polypeptides are useful to
CC	induce angiogenesis e.g wound healing; in the treatment of sports-related
CC	joint problems, articular cartilage defects, osteoarthritis or rheumatoid
CC	arthritis; diabetes; hyperinsulinaemia and hypoinsulinaemia. The
CC	antibodies may be used in various diagnostic, competitive binding and/or
CC	immunoprecipitation assays. The present sequence represents a cDNA
CC	encoding a PRO polypeptide of the invention
XX	
QQ	Sequence 2598 BP; 687 A; 590 C; 648 G; 673 T; 0 U; 0 Other;
	Query Match 98.1%; Score 2514.2; DB 8; Length 2598;
	Best Local Similarity 99.6%; Pred. No. 0;
	Matches 2552; Conservative 0; Mismatches 8; Indels 3; Gaps 3;
QY	1 AGGGGAGCTACACCTCTGGAGCTCAAGATGGTCTTAGTGGGCGCTGTCTTCGAA 60
DB	38 AGGGGAGCTACACCTCTGGAGCTCAAGATGGTCTTAGTGGGCGCTGTCTTCGAA 97
QY	61 TGAAGGACTCGGATTAAGGTGCTTTTATCTGCATATAACCAAGCTTCTAGCTGAGGGC 120
DB	98 TGAAGGACTCGGCATGAAGGTGCTTTATCTGCATATAACCAAGCTTCTAGCTGAGGGC 157
QY	121 TGCATGACGGAAGGTCATTAAAGGTGAAGAGATCAGCGTGGTCCCCAATCGTGGCTGG 180
DB	158 TGCATGACGGAAGGTCATTAAAGGTGAAGAGATCAGCGTGGTCCCCAATCGTGGCTGG 217
QY	181 ATGCCAGCCTGTCCCCCGTCACTCTTGGGTGTCAGGGTGGGAAGCCAGTGCCTGTCTATGTG 240
DB	218 ATGCCAGCCTGTCCCCCGTCACTCTTGGGTGTCAGGGTGGGAAGCCAGTGCCTGTCTATGTG 277
QY	241 GGGTGGGGCAGGAGCCGACTCTAAACATAGAGCCAGTCAAATCATGGAGCTCTATCTTG 300
DB	278 GGGTGGGGCAGGAGCCGACTCTAACTAGAGCCAGTCAAATCATGGAGCTCTATCTTG 337
QY	301 GTGCCAAGGAATCCAAGAGCTTCACCTTCTACCGCGGGGAATGGGGCTCACTCCAGCT 360
DB	338 GTGCCAAGGAATCCAAGAGCTTCACCTTCTACCGCGGGGAATGGGGCTCACTCCAGCT 397
QY	361 TCGAGTCGGCTGCCTACCCGGGCTGGTTCCTGTGCACCGTGCCTGAAGCCGATCAGCCCTG 420
DB	398 TCGAGTCGGCTGCCTACCCGGGCTGGTTCCTGTGCACCGTGCCTGAAGCCGATCAGCCCTG 457
QY	421 TCAGACTCACCACGCTTCCCGAAGATGTGGCTGGAATGCCCCCAATCAGACTTCTACT 480
DB	458 TCAGACTCACCACGCTTCCCGAAGATGTGGCTGGAATGCCCCCAATCAGACTTCTACT 517
QY	481 TCCAGCAGTGTGAATAGGGGAAAGTGCCTCCCGCCAGAACTCCCTGGGCAGAGCCAGTCCG 540
DB	518 TCCAGCAGTGTGAATAGGGGAAAGTGCCTCCCGCCAGAACTCCCTGGGCAGAGCCAGTCCG 576
QY	541 GTGAGGGGTGAGTGAGGAGAGCCCAATGGCGGACAATCACTCTTTTGTCTCTCAGGACCCC 600
DB	577 GTGAGGGGTGAGTGAGGAGAGCCCAATGGCGGACAATCACTCTCTCTCTCTCAGGACCCC 636
QY	601 CAGGTCCTCACTAGTGGGCACTGACCACTTTTGTCTTCTGGTTCAGAGTTTGCATAAAATT 660
DB	637 CAGGTCCTCACTAGTGGGCACTGACCACTTTTGTCTTCTGGTTCAGAGTTTGCATAAAATT 696
QY	661 CTGAGATTTGGAGCTCAGTCCAGGGTCTCTCCCGCCACTGGATGGTCTACTGTCTGTGGAAAC 720
DB	697 CTGAGATTTGGAGCTCAGTCCAGGGTCTCTCCCGCCACTGGATGGTCTACTGTCTGTGGAAAC 756
QY	721 CTTGTAAAAACCAATGTGGGGTAAACTGGGAATAACATGAAAAAGATTTCTCTGGGGGTGG 780

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Db 757 CTTGTAAAAACCAATGTGGGTAACCTGGGNAATCAATGAAGATTTCTGTGGGGTGGG 816
Qy 781 GTGGGGAGTGTGGGAATCAATCTCTTAATGGTAAGTGAACAAGTGTACCTCAGGCC 840
Db 817 GTGGGGAGTGTGGGAATCAATCTCTTAATGGTAAGTGAACAAGTGTACCTCAGGCC 876
Qy 841 CGCAGGCCAACCCATCCCCAGTTGAGCCTTATAGGGTCAGTAGCTCTCCACATGAAGTC 900
Db 877 CGCAGGCCAACCCATCCCCAGTTGAGCCTTATAGGGTCAGTAGCTCTCCACATGAAGTC 936
Qy 901 CTCTCACTCACCACTGTGCAGGAGAGGAGGTGCTCATAGAGTCAGGGATCTATGCGCCT 960
Db 937 CTGTCACTCACCACTGTGCAGGAGAGGAGGTGCTCATAGAGTCAGGGATCTATGCGCCT 996
Qy 961 TGGCCCGAGCCCAACCCCTTCCCTTT-ATCTGCCCACTGTGCATATGCTACCTTTCTCTATC 1019
Db 997 TGGCCCGAGCCCAACCCCTTCCCTTTAATCTGCCCACTGTGCATATGCTACCTTTCTCTATC 1056
Qy 1020 TCTTCCCTCATCATCTGTGTGGGCATGAGGAGGTGGTGAATGTCAAGAGAATGGTTGG 1079
Db 1057 TCTTCCCTCATCATCTGTGTGGGCATGAGGAGGTGGTGAATGTCAAGAGAATGGTTGG 1116
Qy 1080 AGCTCAGAGATAAAGATAAGTATGCTGATCCCTTTTAAAAACCCAAAGATACA 1139
Db 1117 AGCTCAGAGATAAAGATAAGTATGCTGATCCCTTTTAAAAACCCAAAGATACA 1176
Qy 1140 ATCAAAATCCCGATGCTGCTCTATTCCTCATGAAAAAGTGTCTATGACATATTGAGAA 1199
Db 1177 ATCAAAATCCCGATGCTGCTCTATTCCTCATGAAAAAGTGTCTATGACATATTGAGAA 1236
Qy 1200 GACCTACTTACAAAGTGGCATATATTGCAATTTATTTAAATAAAGATACCTATTTATA 1259
Db 1237 GACCTACTTACAAAGTGGCATATATTGCAATTTATTTAAATAAAGATACCTATTTATA 1296
Qy 1260 TATTTCTTTATAGAAAAAGTCTGGAGAGTTTACTTCAATGTACCAATGTCAAGGTGG 1319
Db 1297 TATTTCTTTATAGAAAAAGTCTGGAGAGTTTACTTCAATGTACCAATGTCAAGGTGG 1356
Qy 1320 TGGCAGTATAGGTGATTTTTCTTTTAAATCTGTAAATTTATCTGTATTTCTTAAATTTTC 1379
Db 1357 TGGCAGTATAGGTGATTTTTCTTTTAAATCTGTAAATTTATCTGTATTTCTTAAATTTTC 1416
Qy 1380 TCAATGAAGATGAATCTCTGATATAAATAAAGAAAAATTAATCTTGAGGTGAAGCA 1439
Db 1417 TACAATGAAGATGAATCTCTGATATAAATAAAGAAAAATTAATCTTGAGGTGAAGCA 1476
Qy 1440 GAGCAGACATCATCTGTGATTTGCTCAGCCTCCAAATTTCCCAAGATTAATCAAAATTCGA 1499
Db 1477 GAGCAGACATCATCTGTGATTTGCTCAGCCTCCAAATTTCCCAAGATTAATCAAAATTCGA 1536
Qy 1500 ATCGAGCTCTGCTGCTCTGTTGTTGTAGTAGTATCAGGAAACAGATCTCAGCAAAAGC 1559
Db 1537 ATCGAGCTCTGCTGCTCTGTTGTTGTAGTAGTATCAGGAAACAGATCTCAGCAAAAGC 1596
Qy 1560 CACTGAGGAGGAGGCTGTCTGAGTTGTGTGCTGGAATCTCTGCGGTAAAGAACTTAAA 1619
Db 1597 CACTGAGGAGGAGGCTGTCTGAGTTGTGTGCTGGAATCTCTGCGGTAAAGAACTTAAA 1656
Qy 1620 GAACAAAATCATCTGGTAATTTCTTCTAGAGGATCAGCCCCCTGGGATCCAGGC 1679
Db 1657 GAACAAAATCATCTGGTAATTTCTTCTAGAGGATCAGCCCCCTGGGATCCAGGC 1716
Qy 1680 ATTGGATCCAGTCTCTAAGAAGGCTGCTGTACTGTGTTGAATTTGTGCCCTCAAAATTCGA 1739
Db 1717 ATTGGATCCAGTCTCTAAGAAGGCTGCTGTACTGTGTTGAATTTGTGCCCTCAAAATTCGA 1776
Qy 1740 CATCTCTTGGAAATCTCAGTCTGTGAGTTTATTTGGAGATAAGTCTCTGAGATGTAG 1799
Db 1777 CATCTCTTGGAAATCTCAGTCTGTGAGTTTATTTGGAGATAAGTCTCTGAGATGTAG 1836
Qy 1800 TTAGTTAAGACAAGTCTCTGGATGAAGGTAGACCTTAAATCAATATGACTGGTTTCC 1859
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Db 1837 TTAGTTAAGACAAGTCTATGCTGGATGAAGGTAGACCTAAATTCATATGACTGGTTTC 1896
Qy 1860 TTGTATGAAAAAGAGAGGACACAGACAGAGAGAGCGGGGAAGACTATATGTAAGATG 1919
Db 1897 TTGTATGAAAAAGAGAGGACACAGACAGAGAGAGCGGGGAAGACTATATGTAAGATG 1956
Qy 1920 AAGGCAGAGATCGGAGTTTTCAGGCACACAAGCTTAAGAAAACCAAGATTTGTGGCAACCA 1979
Db 1957 AAGGCAGAGATCGGAGTTTTCAGGCACACAAGCTTAAGAAAACCAAGATTTGTGGCAACCA 2016
Qy 1980 TCAGAAGCTTGAAGAGGCAAGAAATTTCTCCCTAGAGGCTTTAGAGGGATTAACGGC 2039
Db 2017 TCAGAAGCTTGAAGAGGCAAGAAATTTCTCCCTAGAGGCTTTAGAGGGATTAACGGC 2076
Qy 2040 TCTGCTGAAAACCTTAATCTCAGACTTCCAGCCTCTCTGAACGAAGAAGATAAATTCGG 2099
Db 2077 TCTGCTGAAAACCTTAATCTCAGACTTCCAGCCTCTCTGAACGAAGAAGATAAATTCGG 2136
Qy 2100 CTGTTTAAAGCCACCAAGGATAATTTGGTTACAGCAGCTCTAGGAACTAATACAGCTGCT 2159
Db 2137 CTGTTTAAAGCCACCAAGGATAATTTGGTTACAGCAGCTCTAGGAACTAATACAGCTGCT 2196
Qy 2160 AAAATGATCCCTGCTCTCTCTGTTTACATTTCTGTGTGTGCCCTCCCAATGTACCA 2219
Db 2197 AAAATGATCCCTGCTCTCTCTGTTTACATTTCTGTGTGTGCCCTCCCAATGTACCA 2256
Qy 2220 AAGTTGTCTTTGTGACCCCAATAGAATATGCGCAAGTATGGCATGCCACTTCCAAAGATT 2279
Db 2257 AAGTTGTCTTTGTGA-CCAATAGAATATGCGCAAGTATGGCATGCCACTTCCAAAGATT 2315
Qy 2280 AAGTTTAAAGACACATGACGCTTCTACTTGTGAGCCCTCTCTCTGCGCACCACCGCCCC 2339
Db 2316 AAGTTTAAAGACACATGACGCTTCTACTTGTGAGCCCTCTCTCTGCGCACCACCGCCCC 2375
Qy 2340 CAATCTATCTTGGCTCACTCGCTCTGCGGGAAGCTAGTGCCTATGTATGAGCAGGCCTA 2399
Db 2376 CAATCTATCTTGGCTCACTCGCTCTGCGGGAAGCTAGTGCCTATGTATGAGCAGGCCTA 2435
Qy 2400 TAAAGAGACTTACGTGTTAAAAAATGAAGTCTCTGCCACACAGCCACATTAGTGAACCTA 2459
Db 2436 TAAAGAGACTTACGTGTTAAAAAATGAAGTCTCTGCCACACAGCCACATTAGTGAACCTA 2495
Qy 2460 GAAGCAGACATCTGTGAGATAATCGATGTTTGTGTTTAAAGTTGCTCAGTTTGGTCT 2519
Db 2496 GAAGCAGACATCTGTGAGATAATCGATGTTTGTGTTTAAAGTTGCTCAGTTTGGTCT 2555
Qy 2520 AACTTGTATGAGCAATAGATAAATAATATGCAGAGAAGAG 2562
Db 2556 AACTTGTATGAGCAATAGATAAATAATATGCAGAGAAGAG 2598
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## RESULT 10

ACA64061  
ID ACA64061 standard; cDNA; 2598 BP.

XX ACA64061;

XX AC  
XX XX  
DT 16-JUN-2003 (first entry)

XX cDNA encoding human PRO polypeptide #76.

XX Human; PRO polypeptide; secreted and transmembrane protein;  
KW anti-PRO antibody; diagnostic assay; gene expression; gene; ss.

OS Homo sapiens.

XX US2002182638-A1.

PN 05-DEC-2002.

XX 02-MAY-2002; 2002US-00063547.

XX 30-DEC-1998; 98KR-00062142.

PR 08-MAR-1999; 99WO-US005028.  
PR 14-MAY-1999; 99US-00311832.  
PR 14-MAY-1999; 99WO-US010733.  
PR 25-AUG-1999; 99US-00380137.  
PR 25-AUG-1999; 99US-00380138.  
PR 25-AUG-1999; 99US-00380139.  
PR 25-AUG-1999; 99US-00380142.  
PR 15-SEP-1999; 99US-00397342.  
PR 18-OCT-1999; 99US-00403297.  
PR 12-NOV-1999; 99US-00423844.  
PR 30-DEC-1999; 99WO-US031274.  
PR 01-FEB-2000; 2000WO-US004341.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 22-AUG-2000; 2000US-00644848.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 18-SEP-2000; 2000US-00664610.  
PR 18-SEP-2000; 2000US-00665350.  
PR 08-NOV-2000; 2000US-00709238.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 22-MAR-2001; 2001US-00816744.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 30-MAY-2001; 2001US-00870574.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 29-JUN-2001; 2001US-00869599.  
PR 18-JUL-2001; 2001US-00908827.  
PR 06-DEC-2001; 2001US-00006867.  
XX (GETH ) GENENTECH INC.  
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
XX P-PSDB; ABU72362.  
XX WPI; 2003-328612/04.  
DR DR  
DR DR  
XX An isolated secreted transmembrane polypeptide designated PRO, useful as  
XX a therapeutic agent.  
XX Disclosure; Fig 151; 236pp; English.  
XX The present invention relates to the isolation of novel human PRO  
XX polypeptides, and the polynucleotide sequences encoding them. The PRO  
XX polypeptides are secreted and transmembrane proteins. The PRO  
XX polypeptides and polynucleotides are useful for preparing a medicament  
XX useful in the treatment of a condition responsive to anti-PRO antibody.  
XX Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting  
XX its expression in specific cells, tissues or serum, and for affinity  
XX purification of PRO from recombinant cell culture or natural sources.  
XX AC63986-AC64069 represent cDNA sequences encoding the human PRO  
XX polypeptides of the invention  
SQ Sequence 2598 BP; 687 A; 590 C; 648 G; 673 T; 0 U; 0 Other;  
Query Match 98.1%; Score 2514.2; DB 8; Length 2598;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 2552; Conservative 0; Mismatches 8; Indels 3; Gaps 3;  
QY 1 AGGGGAGTCTACACCTGTGGAGCTCAAGATGGTCTCTGAGTGGGGCGCTGTGCTTCGGAA 60  
DB 38 AGGGGAGTCTACACCTGTGGAGCTCAAGATGGTCTCTGAGTGGGGCGCTGTGCTTCGGAA 97  
QY 61 TGAAGACTCGGCATTGAAGGTCCTTTATCTGCATAATAACCAAGCTTCTAGCTGGAGGC 120  
|||||

DB 98 TGAAGACTCGGCATTGAAGGTCCTTTATCTGCATAATAACCAAGCTTCTAGCTGGAGGC 157  
QY 121 TGCATGCAAGGAGAGTCAATTAAGGTGAAGAGATCAGCGTGGTCCCAATCGTGGCTGG 180  
DB 158 TGCATGCAAGGAGAGTCAATTAAGGTGAAGAGATCAGCGTGGTCCCAATCGTGGCTGG 217  
QY 181 ATGCCAGGCTGTCCCGGTCATCTGGGTGTCCAGGGTGAAGAGCCAGTGCCTGTATGTG 240  
DB 218 ATGCCAGGCTGTCCCGGTCATCTGGGTGTCCAGGGTGAAGAGCCAGTGCCTGTATGTG 277  
QY 241 GGGTGGGCGAGAGCCGAGCTCTAACACTAGAGCAGTGAACATCATGTAGAGCTCTATCTTG 300  
DB 278 GGGTGGGCGAGAGCCGAGCTCTAACACTAGAGCAGTGAACATCATGTAGAGCTCTATCTTG 337  
QY 301 GTGCCAAGGAATCCAAGAGCTTCACTTCTACCGCGGGGACATGGGGTCACTCCAGCT 360  
DB 338 GTGCCAAGGAATCCAAGAGCTTCACTTCTACCGCGGGGACATGGGGTCACTCCAGCT 397  
QY 361 TCGAGTCCGGTCCCTACCGGGCTGGTTCCTGTGCACGGTGCCTGAAGCCGATCAGCCTG 420  
DB 398 TCGAGTCCGGTCCCTACCGGGCTGGTTCCTGTGCACGGTGCCTGAAGCCGATCAGCCTG 457  
QY 421 TCAGACTCACCAGCTTCCCGAGAAATGGTGGCTGAATGCCCCCATCACAGACTTCTACT 480  
DB 458 TCAGACTCACCAGCTTCCCGAGAAATGGTGGCTGAATGCCCCCATCACAGACTTCTACT 517  
QY 481 TCCAGCAGTGTGACTAGGGCAACGTGCCCGGGGCAATGAGTGCCTCCCTGGGCGAGAGCAGCTGG 540  
DB 518 TCCAGCAGTGTGACTAGGGCAACGTGCCCGGGGCAATGAGTGCCTCCCTGGGCGAGAGCAGCTGG 576  
QY 541 GTGAGGGGTGAGTGAGAGAGACCCATGGCGGACATCACTCTTTCTGTCTCAGGACCCC 600  
DB 577 GTGAGGGGTGAGTGAGAGAGACCCATGGCGGACATCACTCTCTCTGTCTCAGGACCCC 636  
QY 601 CAGGTCTGACTAGTGGGCAACGTGCCCGGGGCAATGAGTGCCTCCCTGGGCGAGAGTTCATATAAAT 660  
DB 637 CAGGTCTGACTAGTGGGCAACGTGCCCGGGGCAATGAGTGCCTCCCTGGGCGAGAGTTCATATAAAT 696  
QY 661 CTGAGATTTGGAGCTCAGTCCAGGGTCTCCCGGGGCAATGAGTGCCTCCCTGGGCGAGAGTTCATATAAAT 720  
DB 697 CTGAGATTTGGAGCTCAGTCCAGGGTCTCCCGGGGCAATGAGTGCCTCCCTGGGCGAGAGTTCATATAAAT 756  
QY 721 CTTGTAAAAACCATGTGGGGTAAACTGGGATAAATGAGGAGATTTCTGTGGGGGTGGG 780  
DB 757 CTTGTAAAAACCATGTGGGGTAAACTGGGATAAATGAGGAGATTTCTGTGGGGGTGGG 816  
QY 781 GTGGGGGAGTGTGGGAATCATCTCTGCTTAATGTAACTGACAAAGTGTACCTTGAGCC 840  
DB 817 GTGGGGGAGTGTGGGAATCATCTCTGCTTAATGTAACTGACAAAGTGTACCTTGAGCC 876  
QY 841 CCGCAGGCGCAACCCCATCCCGAGTTCAGGCTTATAGGGTCAAGTGTCTCCACATGAAGTC 900  
DB 877 CCGCAGGCGCAACCCCATCCCGAGTTCAGGCTTATAGGGTCAAGTGTCTCCACATGAAGTC 936  
QY 901 CTCTCACTACCACTGTGAGAGAGAGGGGTGATAGAGTCAAGTCAAGGATCTATGGCCCT 960  
DB 937 CTGTCACTCACCACCTGTGAGAGAGAGGGGTGATAGAGTCAAGTCAAGGATCTATGGCCCT 996  
QY 961 TGGCCCGAGCCCGAGCCCGCTTCCCTTT-ATCCTGCCACTGTGCATATGCTACCTTCTCTATC 1019  
DB 997 TGGCCCGAGCCCGAGCCCGCTTCCCTTTAATCTGCCACTGTGCATATGCTACCTTCTCTATC 1056  
QY 1020 TCTTCCCTCATCATCTTGTGTGGGCGATGAGAGGTGGTGTGATGTGAGAGAAATGGTTCG 1079  
DB 1057 TCTTCCCTCATCATCTTGTGTGGGCGATGAGAGGTGGTGTGATGTGAGAGAAATGGTTCG 1116  
QY 1080 AGCTCAGAAGATAAAGATAAGTAGGGTATGCTGATCTCTTTTAAAAACCCCAAGATACA 1139  
DB 1117 AGCTCAGAAGATAAAGATAAGTAGGGTATGCTGATCTCTTTTAAAAACCCCAAGATACA 1176  
QY 1140 ATCAAAATCCAGAGTGGTCTCTATTCCCATGAAGAGTGTCTCATGACATATTGAGAA 1199  
DB 1177 ATCAAAATCCAGAGTGGTCTCTATTCCCATGAAGAGTGTCTCATGACATATTGAGAA 1236

QY 1200 GACCTACTTACAAAGTGGCATATATTGCAATTTATTTTAAATTAAGAATACCTATTATATA 1259  
DB 1237 GACCTACTTACAAAGTGGCATATATTGCAATTTATTTTAAATTAAGAATACCTATTATATA 1296  
QY 1260 TATTTCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTTGTAGCAATGTCAGGGTGG 1319  
DB 1297 TATTTCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTTGTAGCAATGTCAGGGTGG 1356  
QY 1320 TGGCAGTATAGGTGATTTTTCTTTTAAATTTCTGTTAATTTATCTGTATTTTCTTAAATTTTC 1379  
DB 1357 TGGCAGTATAGGTGATTTTTCTTTTAAATTTCTGTTAATTTATCTGTATTTTCTTAAATTTTC 1416  
QY 1380 TACAATGAAGATGAATCTCTGTATTAATAAATAAGAAAAAATAATTAATCTTGAGGTAAAGCA 1439  
DB 1417 TACAATGAAGATGAATCTCTGTATTAATAAATAAGAAAAAATAATTAATCTTGAGGTAAAGCA 1476  
QY 1440 GAGCAGACATCATCTGTATTCCTCAGCTCCCAATCCCGAGAGTAATTCAAATTCGA 1499  
DB 1477 GAGCAGACATCATCTGTATTCCTCAGCTCCCAATCCCGAGAGTAATTCAAATTCGA 1536  
QY 1500 ATCGAGCTCTGCTGCTCTGTTGTTGTAGTAGTATCAGGAAACAGATCTCAGCAAAGC 1559  
DB 1537 ATCGAGCTCTGCTGCTCTGTTGTTGTAGTAGTATCAGGAAACAGATCTCAGCAAAGC 1596  
QY 1560 CACTGAGGAGGAGGCTGCTGAGTTTGTGTGGTGAATCTCTGGGTAAAGAACTTAAA 1619  
DB 1597 CACTGAGGAGGAGGCTGCTGAGTTTGTGTGGTGAATCTCTGGGTAAAGAACTTAAA 1656  
QY 1620 GAACAAAAATCATCTGTTAATTTCTTCTAGAAAGATCAGCCCTGGGATTCAGAGC 1679  
DB 1657 GAACAAAAATCATCTGTTAATTTCTTCTAGAAAGATCAGCCCTGGGATTCAGAGC 1716  
QY 1680 ATTGATCCAGTCTTAAGAAGCTGCTGCTACTGTTGTAATTTGTGCTCCCTCAAAATTCGA 1739  
DB 1717 ATTGATCCAGTCTTAAGAAGCTGCTGCTACTGTTGTAATTTGTGCTCCCTCAAAATTCGA 1776  
QY 1740 CATCTCTTTGGAATCTCAGTCTGTGAGTTTATTTGGAGATAAGGTCTCTGAGATGTAG 1799  
DB 1777 CATCTCTTTGGAATCTCAGTCTGTGAGTTTATTTGGAGATAAGGTCTCTGAGATGTAG 1836  
QY 1800 TTAGTTAAGCAAGGTCTGCTGGATGAAGGTAGACCTAAATCAATATGACTGTTTCC 1859  
DB 1837 TTAGTTAAGCAAGGTCTGCTGGATGAAGGTAGACCTAAATCAATATGACTGTTTCC 1896  
QY 1860 TTGTATGAAGAGGAGGACACAGACAGAGAGGAGCGGGGAGACTATGTAAAGATG 1919  
DB 1897 TTGTATGAAGAGGAGGACACAGACAGAGAGGAGCGGGGAGACTATGTAAAGATG 1956  
QY 1920 AAGGCAGAGATCGGAGTTTTCAGGCCACAAGCTTAAGAAACACCAAGGATGTGGCAACCA 1979  
DB 1957 AAGGCAGAGATCGGAGTTTTCAGGCCACAAGCTTAAGAAACACCAAGGATGTGGCAACCA 2016  
QY 1980 TCAGAAGCTTGAAGAGGCAAGAAATCTTCTCCTAGAGGCTTTAGAGGATTAACGGC 2039  
DB 2017 TCAGAAGCTTGAAGAGGCAAGAAATCTTCTCCTAGAGGCTTTAGAGGATTAACGGC 2076  
QY 2040 TCTGCTGAAACCTTAATCTCAGACTTCCAGCTCTGAGCGAAGAGAAATTAATTTCCG 2099  
DB 2077 TCTGCTGAAACCTTAATCTCAGACTTCCAGCTCTGAGCGAAGAGAAATTAATTTCCG 2136  
QY 2100 CTGTTTAAAGCCACCAAGGATTAATGGTTTACAGCAGCTCTAGGAAACTAATACAGCTGCT 2159  
DB 2137 CTGTTTAAAGCCACCAAGGATTAATGGTTTACAGCAGCTCTAGGAAACTAATACAGCTGCT 2196  
QY 2160 AAAATGATCCCTGTCTCTCGTGTGTATTTACATTTCTGTGTGTGTCCTCCACCAATGTACCA 2219  
DB 2197 AAAATGATCCCTGTCTCTCGTGTGTATTTACATTTCTGTGTGTGTCCTCCACCAATGTACCA 2256  
QY 2220 AAGTTCTTTTGTGACCCCAATAGATATGCGAGAGTGTGGCATGCCACTTCCAGATT 2279  
DB 2257 AAGTTCTTTTGTGA-CCAATAGATATGCGAGAGTGTGGCATGCCACTTCCAGATT 2315

QY 2280 AGGTTATAAAGACACTGCAGCTTCTACTTTAGCCCTCTCTCTGCGACCCACCGCCCC 2339  
DB 2316 AGGTTATAAAGACACTGCAGCTTCTACTTTAGCCCTCTCTCTGCGACCCACCGCCCC 2375  
QY 2340 CAATCTATCTTGGCTCACTCGCTCTGGGGAAAGCTAGCTGCCATGCTATGAGCAGGCCTA 2399  
DB 2376 CAATCTAICTTGGCTCACTCGCTCTGGGGAAAGCTAGCTGCCATGCTATGAGCAGGCCTA 2435  
QY 2400 TAAAGAGACTTACGTGGTTAAAAAATGAAGTCTCTGCCCCACAGCCACATTAGTGAACCTA 2459  
DB 2436 TAAAGAGACTTACGTGGTTAAAAAATGAAGTCTCTGCCCCACAGCCACATTAGTGAACCTA 2495  
QY 2460 GAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTAAAGTTGCTCAGTTTGGTCT 2519  
DB 2496 GAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTAAAGTTGCTCAGTTTGGTCT 2555  
QY 2520 AACTTGTATGAGCAATAGATAAATAATATGAGAGAAAGAG 2562  
DB 2556 AACTTGTATGAGCAATAGATAAATAATATGAGAGAAAGAG 2598

RESULT 11  
ACA91325  
ID ACA91325 standard; cdna; 2598 BP.  
XX  
AC ACA91325;  
XX  
DT 14-JUL-2003 (first entry)  
XX  
DE cdna encoding human PRO polypeptide #76.  
XX  
KW Human; PRO polypeptide; secreted protein; transmembrane protein; rectal;  
KW lung; stomach; oesophageal; skin; tumour; cancer; cytostatic;  
KW gene therapy; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2003018168-A1.  
XX  
PD 23-JAN-2003.  
XX  
PF 02-MAY-2002; 2002US-00063569.  
XX  
PR 30-DEC-1998; 98KR-00062142.  
PR 08-MAR-1999; 99WO-US005028.  
PR 14-MAY-1999; 99US-00311832.  
PR 14-MAY-1999; 99WO-US010733.  
PR 25-AUG-1999; 99US-00380137.  
PR 25-AUG-1999; 99US-00380138.  
PR 25-AUG-1999; 99US-00380139.  
PR 25-AUG-1999; 99US-00380142.  
PR 15-SEP-1999; 99US-00397342.  
PR 18-OCT-1999; 99US-00403297.  
PR 12-NOV-1999; 99US-00423844.  
PR 30-DEC-1999; 99WO-US031274.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 22-AUG-2000; 2000US-00644848.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 18-SEP-2000; 2000US-00664610.  
PR 18-SEP-2000; 2000US-00665350.  
PR 08-NOV-2000; 2000US-00709238.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 22-MAR-2001; 2001US-00816744.  
PR 10-MAY-2001; 2001US-00854208.





Db 1597 CACTGAGGAGGCTGTGCTGAGTTTGTGCTGGAATCTCTGGTAAGGAACCTTAA 1656  
Qy 1620 GAACAAAAATCATCTGGTAATCTTTCTTAGAAGGATCAAGCCCTGGGATTCGAAGGC 1679  
Db 1657 GAACAAAAATCATCTGGTAATCTTTCTTAGAAGGATCAAGCCCTGGGATTCGAAGGC 1716  
Qy 1680 ATTGGATCCAGTCTCTAAGAAGGCTGCTACTGTTGTAATTTGTCCTCCCTCAATTTCA 1739  
Db 1717 ATTGGATCCAGTCTCTAAGAAGGCTGCTACTGTTGTAATTTGTCCTCCCTCAATTTCA 1776  
Qy 1740 CATCTCTCTTGAATCTCTAGTCTGTGAGTTTATTTGGAGATAAGGTCTCTGAGATGTAG 1799  
Db 1777 CATCTCTCTTGAATCTCTAGTCTGTGAGTTTATTTGGAGATAAGGTCTCTGAGATGTAG 1836  
Qy 1800 TTAGTTAAGCAAGGTCATCTGGATGAAGGTAGACCTAAATTCATATGACTGTTTCC 1859  
Db 1837 TTAGTTAAGCAAGGTCATCTGGATGAAGGTAGACCTAAATTCATATGACTGTTTCC 1896  
Qy 1860 TTGTATGAAGAGGAGGACACAGACACAGAGAGAGCGGGGAGACTATGTAAGATG 1919  
Db 1897 TTGTATGAAGAGGAGGACACAGACACAGAGAGAGCGGGGAGACTATGTAAGATG 1956  
Qy 1920 AAGGCAGAGATCGGAGTTTTCAGGCCCAAGCTTAAGAAAACCAAGGATTTGGCAACCA 1979  
Db 1957 AAGGCAGAGATCGGAGTTTTCAGGCCCAAGCTTAAGAAAACCAAGGATTTGGCAACCA 2016  
Qy 1980 TCAGAAGCTTGAAGAGCAAGAAATCTTCCCTAGAGGCTTTAGAGGATTAACGGC 2039  
Db 2017 TCAGAAGCTTGAAGAGCAAGAAATCTTCCCTAGAGGCTTTAGAGGATTAACGGC 2076  
Qy 2040 TCTGCTGAACCTTAATCTCAGACTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCG 2099  
Db 2077 TCTGCTGAACCTTAATCTCAGACTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCG 2136  
Qy 2100 CTGTTTAAAGCACCAGGATAATTTGTTACAGAGCTCTAGAGAACTAATACAGCTGCT 2159  
Db 2137 CTGTTTAAAGCACCAGGATAATTTGTTACAGAGCTCTAGAGAACTAATACAGCTGCT 2196  
Qy 2160 AAAATGATCCCTGTCTCTCGTGTTTTACATTTCTGTGTGTCTCCCTCCCAATGTACCA 2219  
Db 2197 AAAATGATCCCTGTCTCTCGTGTTTTACATTTCTGTGTGTCTCCCTCCCAATGTACCA 2256  
Qy 2220 AAGTTGCTTTGTGACCAATAGATATGGCAGAGTGTGGATGCGCATCTTCCAGATT 2279  
Db 2257 AAGTTGCTTTGTGA-CCAATAGATATGGCAGAGTGTGGATGCGCATCTTCCAGATT 2315  
Qy 2280 AGTTTATAAAGACACTGAGCTTCTACTTTGAGCCCTCTCTCTGCGCACCCACCGCC 2339  
Db 2316 AGTTTATAAAGACACTGAGCTTCTACTTTGAGCCCTCTCTCTGCGCACCCACCGCC 2375  
Qy 2340 CAATCTATCTTGGCTCACTCGCTCTGGGGAAGCTAGCTGCCATGCTATGAGCGCCTA 2399  
Db 2376 CAATCTATCTTGGCTCACTCGCTCTGGGGAAGCTAGCTGCCATGCTATGAGCGCCTA 2435  
Qy 2400 TAAAGAGACTTACGTGGTAAAAAATGAAGTCTCTGCGCACCCACCATATTAGTAACCTA 2459  
Db 2436 TAAAGAGACTTACGTGGTAAAAAATGAAGTCTCTGCGCACCCACCATATTAGTAACCTA 2495  
Qy 2460 GAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTAAAGTTGCTCAGTTTGGTCT 2519  
Db 2496 GAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTAAAGTTGCTCAGTTTGGTCT 2555  
Qy 2520 AACTTGTATGAGCAATAGATAAATAATATGAGAGAAAGAG 2562  
Db 2556 AACTTGTATGAGCAATAGATAAATAATATGAGAGAAAGAG 2598

RESULT 12  
ACD45224

ID ACD45224 standard; cDNA; 2598 BP.

XX AC ACD45224;

XX

DT 11-SEP-2003 (first entry)

XX Human secreted/transmembrane polypeptide PRO4342 cDNA.

XX Human; ss; tumour; cancer; gene therapy; tissue typing; gene.

XX Homo sapiens.

OS US2003009012-A1.

XX 09-JAN-2003.

XX 01-MAY-2002; 2002US-00063517.

XX 30-DEC-1998; 98KR-00062142.

XX 08-MAR-1999; 99WO-US005028.

XX 14-MAY-1999; 99US-00311832.

XX 25-AUG-1999; 99WO-US010733.

XX 25-AUG-1999; 99US-00380137.

XX 25-AUG-1999; 99US-00380138.

XX 25-AUG-1999; 99US-00380139.

XX 15-SEP-1999; 99US-00397342.

XX 18-OCT-1999; 99US-00403297.

XX 12-NOV-1999; 99US-00423844.

XX 30-DEC-1999; 99WO-US031274.

XX 18-FEB-2000; 2000WO-US004341.

XX 01-MAR-2000; 2000WO-US005601.

XX 02-MAR-2000; 2000WO-US005841.

XX 21-MAR-2000; 2000WO-US007532.

XX 22-MAY-2000; 2000WO-US014042.

XX 02-JUN-2000; 2000WO-US015264.

XX 22-AUG-2000; 2000US-00644848.

XX 24-AUG-2000; 2000WO-US023328.

XX 18-SEP-2000; 2000US-00664610.

XX 18-SEP-2000; 2000US-00665350.

XX 08-NOV-2000; 2000US-00709238.

XX 10-NOV-2000; 2000WO-US030873.

XX 01-DEC-2000; 2000WO-US032678.

XX 20-DEC-2000; 2000US-00747259.

XX 20-DEC-2000; 2000WO-US034956.

XX 28-FEB-2001; 2001WO-US006520.

XX 22-MAR-2001; 2001US-00816744.

XX 10-MAY-2001; 2001US-00854208.

XX 30-MAY-2001; 2001US-00854280.

XX 01-JUN-2001; 2001US-00870574.

XX 05-JUN-2001; 2001WO-US017800.

XX 29-JUN-2001; 2001US-00874503.

XX 18-JUL-2001; 2001US-00908827.

XX 06-DEC-2001; 2001US-00006867.

(GETH ) GENENTECH INC.

Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;

Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

WPI; 2003-447383/42.

P-PSDB; ABO27356.

New isolated antibody specifically binding a PRO polypeptide, useful for the preparation of a medicament for treating disorders with the aberrant expression or activity of the PRO polypeptide, such as tumor conditions and cancer.

Dislosure; Fig 151; 223pp; English.

The invention relates to an antibody that binds to a secreted and transmembrane PRO polypeptide. The methods and compositions of the present invention are useful for the preparation of a medicament for the treatment of disorders associated with the aberrant expression or activity of the PRO polypeptide, such as tumour conditions and cancer. They can also be used to generate transgenic or knockout animals useful



CC in the development and screening of therapeutically useful reagents. The  
CC PRO polypeptides and encoding nucleic acids can be used as molecular  
CC weight markers for protein electrophoresis, chromosome identification and  
CC tissue typing. The antibodies may be used in various diagnostic,  
CC competitive binding and/or immunoprecipitation assays. The present  
CC sequence represents a secreted and transmembrane PRO polypeptide cDNA  
XX  
SQ Sequence 2598 BP; 687 A; 590 C; 648 G; 673 T; 0 U; 0 Other;

[illegible]

```
Db 2017 TCAGAGCTTGAAGAGCGAAGAGAAATCTTCCTAGAGGCTTTAGAGGATTAACGGC 2076
Qy TCTGCTGAACCTTAATCTCAGACTTCCAGCTCTCCGAAACGAAAGAAATAAATTTTCGG 2099
Db TCTGCTGAACCTTAATCTCAGACTTCCAGCTCTCCGAAACGAAAGAAATAAATTTTCGG 2136
Qy CTGTTTAAAGCCACCAAGATAATTTGTTACAGCAGCTCTAGAAACTTAATACAGCTGCT 2159
Db CTGTTTAAAGCCACCAAGATAATTTGTTACAGCAGCTCTAGAAACTTAATACAGCTGCT 2196
Qy AAAATGATCCCTGCTCTCCTCGTGTTCATATCTGTGTGTGTCCTCCACAAATGTACCA 2219
Db AAAATGATCCCTGCTCTCCTCGTGTTCATATCTGTGTGTGTCCTCCACAAATGTACCA 2256
Qy AAGTTGTCTTTGTGACCCCAATAGATATGCGCAGAGTGTATGGCATGCCACTTCCAAAGATT 2279
Db AAGTTGTCTTTGTGACCCCAATAGATATGCGCAGAGTGTATGGCATGCCACTTCCAAAGATT 2315
Qy AGTTTATAAAGACACTGAGCTTCTA CTTGAGCCCTCTCTCTGCGCACCCACCGCCGCC 2339
Db AGTTTATAAAGACACTGAGCTTCTA CTTGAGCCCTCTCTCTGCGCACCCACCGCCGCC 2375
Qy CAATCTATCTTGGCTCACTCGCTCTGGGGGAAGTAGTGCCTATGAGCAGGCCCTA 2399
Db CAATCTATCTTGGCTCACTCGCTCTGGGGGAAGTAGTGCCTATGAGCAGGCCCTA 2435
Qy TAAAGAGACTTACGTGGTAAATAAAGTCTCTGCGCCACAGCCACATAGTGAACCTA 2459
Db TAAAGAGACTTACGTGGTAAATAAAGTCTCTGCGCCACAGCCACATAGTGAACCTA 2495
Qy GAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTAAAGTTGCTCAGTTTGGTCT 2519
Db GAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTAAAGTTGCTCAGTTTGGTCT 2555
Qy AACTTGTATGAGCAATAGATAAATAATATATCAGAGAAAGAG 2562
Db AACTTGTATGAGCAATAGATAAATAATATATCAGAGAAAGAG 2598

RESULT 13
ACA93772
ID ACA93772 standard; cDNA; 2598 BP.
AC ACA93772;
XX
XX
XX
XX
XX 17-JUL-2003 (first entry)
XX
XX Human cDNA encoding secreted/transmembrane protein PRO4342.
XX Human; ss; Gene; PRO; secreted protein; transmembrane protein;
XX cytosolic; vulnary; osteopathic; antiarthritic; antirheumatic;
XX lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour;
XX liver tumour; tumour necrosis factor; pericyte cell proliferation;
XX TNF-alpha; proteoglycans release; cartilage; cancer; wound healing;
XX cartilage defect; osteoarthritis; rheumatoid arthritis.
XX
XX Homo sapiens.
XX
XX US2003045684-A1.
XX
XX
XX PD 06-MAR-2003.
XX
XX PF 02-MAY-2002; 2002US-00053553.
XX
XX PR 30-DEC-1998; 98KR-00052142.
XX PR 08-MAR-1999; 99WO-US095028.
XX PR 14-MAY-1999; 99US-00311832.
XX PR 14-MAY-1999; 99WO-US010733.
XX PR 25-AUG-1999; 99US-00380137.
XX PR 25-AUG-1999; 99US-00380138.
XX PR 25-AUG-1999; 99US-00380139.
XX PR 25-AUG-1999; 99US-00380142.
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PR 15-SEP-1999; 99US-00397342.
PR 18-OCT-1999; 99US-00403297.
PR 12-NOV-1999; 99US-00423844.
PR 30-DEC-1999; 99WO-US031274.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000WO-US007532.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-AUG-2000; 2000WO-US023328.
PR 24-AUG-2000; 2000US-0064610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-0074259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 30-MAY-2001; 2001US-00870574.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 29-JUN-2001; 2001US-00869599.
PR 18-JUL-2001; 2001US-00908827.
PR 06-DEC-2001; 2001US-00006867.
XX
XX (GETH ) GENENTECH INC.
XX
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
XX WPI; 2003-392892/37.
XX P-PSDB; ABU92551.
XX
XX New PRO994 polypeptide, useful for detecting tumors, or for stimulating
XX Tumor Necrosis Factor alpha, or pericyte proliferation, especially for
XX treating cancer, cartilage defects, osteoarthritis and rheumatoid
XX arthritis in a mammal.
XX
XX Disclosure; Fig 151; 235pp; English.
XX
XX The invention relates to a new isolated PRO994 polypeptide comprises an
XX amino acid sequence appearing as ABU92499, PRO994 lacking its associated
XX signal peptide, the extracellular domain of PRO994, the extracellular
XX domain of PRO994 (lacking it associated signal peptide) or the protein
XX encoded by the full-length coding sequence of the cDNA ATCC 203018. Also
XX included is a chimaeric molecule comprising the PRO994 polypeptide fused
XX to a heterologous amino acid sequence. The PRO polypeptide is useful in
XX pharmaceuticals, diagnostics, biosensors or bioreactors. It is
XX particularly useful for detecting tumors (e.g. lung tumour, colon
XX tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)
XX in a mammal, for stimulating the release of tumour necrosis factor (TNF)-
XX alpha from human blood, for stimulating the proliferation of pericyte
XX cells, or stimulating the release of proteoglycans from cartilage. The
XX polypeptide may be employed for a variety of therapeutic purposes, e.g.
XX for treating cancer, wound healing, cartilage defects, osteoarthritis,
XX rheumatoid arthritis. Also disclosed are the cDNA encoding PRO994, 83
XX other PRO polypeptides and their encoding cDNAs. The present sequence
XX encodes a PRO polypeptide of the invention
XX
XX Sequence 2598 BP; 687 A; 590 C; 648 G; 673 T; 0 U; 0 Other;
XX
XX Query Match 98.1%; Score 2514.2; DB 8; Length 2598;
XX Best Local Similarity 99.6%; Pred. No. 0;
XX Matches 2552; Conservative 0; Mismatches 8; Indels 3; Gaps 3;
XX
XX Qy 1 AGGGGAGTCTACACCTGTGGAGCTCAAGATGCTCTGAGTGGGGCGCTGCTCCGAA 60
XX Db 38 AGGGGAGTCTACACCTGTGGAGCTCAAGATGCTCTGAGTGGGGCGCTGCTCCGAA 97
```

Qy	61	TGAAGGACTCGGCATGGAAGTGTCTTTATCTGCAATAAACCAAGCTTCTAGCTGGAGGC	120
Db	98		
		TGAAGGACTCGGCATGGAAGTGTCTTTATCTGCAATAAACCAAGCTTCTAGCTGGAGGC	157
Qy	121	TGCATGAGGGAAGGTCATTAAAGGTGAAGAGATCAGCGTGGTCCCCAATCGGTGGCTGG	180
Db	158		
		TGCATGAGGGAAGGTCATTAAAGGTGAAGAGATCAGCGTGGTCCCCAATCGGTGGCTGG	217
Qy	181	ATGCCAGCTCTGCCCGTCATCTCGGTGTTCAGGGGTGGAAGCCAGTGCCTGTCAATGTG	240
Db	218		
		ATGCCAGCTCTGCCCGTCATCTCGGTGTTCAGGGGTGGAAGCCAGTGCCTGTCAATGTG	277
Qy	241	GGGTGGGGCAGGAGCCGACTCTAACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG	300
Db	278		
		GGGTGGGGCAGGAGCCGACTCTAACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG	337
Qy	301	GTGCCAAGGAATCAAGAGCTTCACTTTACCGGCGGAGCATGGGGCTCACCTCGAGCT	360
Db	338		
		GTGCCAAGGAATCAAGAGCTTCACTTTACCGGCGGAGCATGGGGCTCACCTCGAGCT	397
Qy	361	TCGAGTCGGCTCGCTACCCGGCTGGTTTCTGTGTCACGGTGCCTGAAGCCGATCAGCGCTG	420
Db	398		
		TCGAGTCGGCTCGCTACCCGGCTGGTTTCTGTGTCACGGTGCCTGAAGCCGATCAGCGCTG	457
Qy	421	TCAGACTCACCCAGCTTCCCAGAGAATGGTGGCTGGAAATGCCCCCATCACAGACTTCTACT	480
Db	458		
		TCAGACTCACCCAGCTTCCCAGAGAATGGTGGCTGGAAATGCCCCCATCACAGACTTCTACT	517
Qy	481	TCCAGCAGTGTGACTAGGGCAACGTGCCCGCCCGAGAACTCCCTGGGCGAGCGAGCTCGG	540
Db	518		
		TCCAGCAGTGTGACTAGGGCAACGTG-CGCCCGAGAACTCCCTGGGCGAGCGAGCTCGG	576
Qy	541	GTGAGGGGTGAGTGGAGGAGACCACTGGCGGAGCAATCACTTTTCTGCTCTCAGGACCCC	600
Db	577		
		GTGAGGGGTGAGTGGAGGAGACCACTGGCGGAGCAATCACTTTTCTGCTCTCAGGACCCC	636
Qy	601	CAGGTCTGACTTAGTGGGCACTGACCACTTTTGTCTTCTGTTCCCAAGTTTGATAAATT	660
Db	637		
		CAGGTCTGACTTAGTGGGCACTGACCACTTTTGTCTTCTGGTCCCAAGTTTGATAAATT	696
Qy	661	CTGAGATTTGGAGTCTAGTCCAGGGTCTCCCCCACTGGATGGTGTCTATGCTGTGGAAAC	720
Db	697		
		CTGAGATTTGGAGTCTAGTCCAGGTCTCCCCCACTGGATGGTGTCTATGCTGTGGAAAC	756
Qy	721	CTTGTAAAAACCATGTGGGTAAACTGGGAAATAACATGAAAGATTTCTGTGGGGGTGGG	780
Db	757		
		CTTGTAAAAACCATGTGGGTAAACTGGGAAATAACATGAAAGATTTCTGTGGGGGTGGG	816
Qy	781	GTGGGGAGTGTGGGAATCATTCCTGCTTAAATGGTAACTGACAAGTGTGTACCTCGAGCC	840
Db	817		
		GTGGGGAGTGTGGGAATCATTCCTGCTTAAATGGTAACTGACNAAGTGTGTACCTCGAGCC	876
Qy	841	CCGAGGCCCAACCCATCCCGAGTTGAGCTTTATAGGGTCAGTAGCTCTCCACATGAATC	900
Db	877		
		CCGAGGCCCAACCCATCCCGAGTTGAGCTTTATAGGGTCAGTAGCTCTCCACATGAATC	936
Qy	901	CTCTCACTCACCATGTGTGCAGGAGGAGGTGTGTATAGAGTCAGGGATCTATGGCCCT	960
Db	937		
		CTGTCACTCACCATGTGTGCAGGAGGAGGTGTGTATAGAGTCAGGGATCTATGGCCCT	996
Qy	961	TGGCCCCAGCCCCACCCCTTCCCTTTT-ATCCTGCCATGTGCATATGCTACTTCTCTATC	1019
Db	997		
		TGGCCCCAGCCCCACCCCTTCCCTTTTAACTCTGCCATGTGCATATGCTACTTCTCTATC	1056
Qy	1020	TCCTTCCCTCATCATCTTGTGTGGGCATGAGGAGGTGGTGAATGTCAAGAAATGTGTTCG	1079
Db	1057		
		TCCTTCCCTCATCATCTTGTGTGGGCATGAGGAGGTGGTGAATGTCAAGAAATGTGTTCG	1116
Qy	1080	AGCTCAGAAGATAAAGATAAGTAGGAGTATGCTGATCCTCTTTTAAAAAAACCAAGATACA	1139
Db	1117		
		AGCTCAGAAGATAAAGATAAGTAGGAGTATGCTGATCCTCTCTTTTAAAAAAACCAAGATACA	1176

1140	ATCAAAATCCAGATGCTGGTCTCTATTTCCCATGAAAAAGTGCCTCATGACATATTCAGAA	1199
1177	ATCAAAATCCAGATGCTGGTCTCTATTTCCCATGAAAAAGTGCCTCATGACATATTCAGAA	1236
1200	GACCTACTTACAAGTGGCATATATTTGCAATTTATTTTAAATTAATAAGATACCTATTTATA	1259
1237	GACCTACTTACAAGTGGCATATATTTGCAATTTATTTTAAATTAATAAGATACCTATTTATA	1296
1260	TATTTCTTTATAGAAAAAGTCTGGAGAGTTTTACTTCCAAATTTGTAGCAATGTCCAGGTGG	1319
1297	TATTTCTTTATAGAAAAAGTCTGGAGAGTTTTACTTCCAAATTTGTAGCAATGTCCAGGTGG	1356
1320	TGGCAGTATAGGTGATTTTCTTTTAAATTTCTGTAAATTTATCTGTATTTTCTAAATTTTTC	1379
1357	TGGCAGTATAGGTGATTTTCTTTTAAATTTCTGTAAATTTATCTGTATTTTCTTAAATTTTTC	1416
1380	TACAAATGAAGATGAATTCCTTGTATATAAAATTAAGAAAGAAATTAATCTTTGAGGTAAAGCA	1439
1417	TACAAATGAAGATGAATTCCTTGTATATAAAATTAAGAAAGAAATTAATCTTTGAGGTAAAGCA	1476
1440	GAGCAGACATCATCTCTGATTTGCTTCAGCCTCCAAATTCACAGAGTAAATTCAAATTTGA	1499
1477	GAGCAGACATCATCTCTGATTTGCTTCAGCCTCCAAATTCACAGAGTAAATTCAAATTTGA	1536
1500	ATCGAGCTCTGCTGCTCTGGTTGGTTGTATGTATGATACAGAAACAGATCTCAGCAAAAGC	1559
1537	ATCGAGCTCTGCTGCTCTGGTTGGTTGTATGTATGATACAGAAACAGATCTCAGCAAAAGC	1596
1560	CACGTGAGGAGGAGGCTGCTGATTTTGTGTGGCTGGAACTCTCGGTAAAGAACTTTAA	1619
1597	CACGTGAGGAGGAGGCTGCTGATTTTGTGTGGCTGGAACTCTCGGTAAAGAACTTTAA	1656
1620	GAACAAAAATCATCTCGTAAATCTTTTCTTAGAAGGATCACAGCCCTCGGAAATTCCAAGGC	1679
1657	GAACAAAAATCATCTCGTAAATCTTTTCTTAGAAGGATCACAGCCCTCGGAAATTCCAAGGC	1716
1680	ATTGGATCCAGTCTCTAAGAAGGCTCTGCTACTGTGGTTGAAATTTGTGTCCTCCCTCAAATTC	1739
1717	ATTGGATCCAGTCTCTAAGAAGGCTCTGCTACTGTGGTTGAAATTTGTGTCCTCCCTCAAATTC	1776
1740	CATCCTTTTGGAAATCTCAGTCTGAGGTTTATTTGGAGATAAGGTCTCTGCAGATGTAG	1799
1777	CATCCTTTTGGAAATCTCAGTCTGAGGTTTATTTGGAGATAAGGTCTCTGCAGATGTAG	1836
1800	TTAGTTAAGACAAGGTCATGCTGGATGAAGGTAGACCTTAAATTTCAATATGACTGGTTTCC	1859
1837	TTAGTTAAGACAAGGTCATGCTGGATGAAGGTAGACCTTAAATTTCAATATGACTGGTTTCC	1896
1860	TTGTATGAAAGAGGAGGACACAGACAGAGGAGACGCGGGGAGACTATGTAAAGATG	1919
1897	TTGTATGAAAGAGGAGGACACAGACAGAGGAGACGCGGGGAGACTATGTAAAGATG	1956
1920	AAGCGAGATCCGAGTTTTCAGCCAAAGCTAAGAAACACCAAGGATTTGGGCAACCA	1979
1957	AAGCGAGATCCGAGTTTTCAGCCAAAGCTAAGAAACACCAAGGATTTGGGCAACCA	2016
1980	TCAGAGCTTTGGAAGAGGCAAGAAATTTCTTCCCTACAGGCTTTTAGAGGGATACGCG	2039
2017	TCAGAGCTTTGGAAGAGGCAAGAAATTTCTTCCCTACAGGCTTTTAGAGGGATACGCG	2076
2040	CTCTGCTGAAACCTTAATCTCAGACTTCACAGCTTCCTGAAACGAAGAAAGAAATTAATTCGG	2099
2077	CTCTGCTGAAACCTTAATCTCAGACTTCACAGCTTCCTGAAACGAAGAAAGAAATTAATTCGG	2136
2100	CTGTTTAAAGCCACCAAGGATAATTTGGTTACAGAGCTCTAGGAAACTTAATCAGCTGCT	2159
2137	CTGTTTAAAGCCACCAAGGATAATTTGGTTACAGAGCTCTAGGAAACTTAATCAGCTGCT	2196
2160	AAATGATCCCTGCTCTCGTGTATTTACATCTCTGTGTGTCCCTCCCAATGTACCA	2219
2197	AAATGATCCCTGCTCTCGTGTATTTACATCTCTGTGTGTCCCTCCCAATGTACCA	2256
2220	AAGTTGCTTTGTGACCAATAGAAATATGGCAGAAGTGTGGCATGCCATCTTCCAAAGATT	2279

```
Db 2257 AGTTGCTTTTGA-CCATAGAAATATGCGAGAGTATGTCATGCCACTTCCAGATT 2315
Qy 2280 AGTTTATAAAGACACTGCAGCTTCTACTTGTAGCCCTCTCTCTCTGCCACCCACGCCCCC 2339
Db 2316 AGTTTATAAAGACACTGCAGCTTCTACTTGTAGCCCTCTCTCTCTGCCACCCACGCCCCC 2375
Qy 2340 CAATCTATCTTGGCTCACTCGCTCTGGGGAGAGCTAGTGCCTATGATGAGGAGCCTA 2399
Db 2376 CAATCTATCTTGGCTCACTCGCTCTGGGGAGAGCTAGTGCCTATGATGAGGAGCCTA 2435
Qy 2400 TAAAGAGACTTACGTGTTAAAAAAGTCTCTCTGCCACGCCACATTAGTGAACCTA 2459
Db 2436 TAAAGAGACTTACGTGTTAAAAAAGTCTCTCTGCCACGCCACATTAGTGAACCTA 2495
Qy 2460 GAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTAAAGTCTCTCAGTTTGGTCT 2519
Db 2496 GAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTAAAGTCTCTCAGTTTGGTCT 2555
Qy 2520 AACTTGTATTGAGCAATAGATAAATAATATGAGAGAAAGAG 2562
Db 2556 AACTTGTATTGAGCAATAGATAAATAATATGAGAGAAAGAG 2598
```

## RESULT 14

ACA67346  
ID ACA67346 standard; cDNA; 2598 BP.

AC ACA67346;

DT 23-JUN-2003 (first entry)

DE cDNA encoding human secreted polypeptide PRO4342.

KW Human; gene; ss; affinity purification.

OS Homo sapiens.

PN US2003027212-A1.

PD 06-FEB-2003.

PF 02-MAY-2002; 2002US-00063544.

PR 30-DEC-1998; 98KR-00062142.

PR 08-MAR-1999; 99WO-US005028.

PR 14-MAY-1999; 99US-00311832.

PR 14-MAY-1999; 99WO-US010733.

PR 25-AUG-1999; 99US-00380137.

PR 25-AUG-1999; 99US-00380138.

PR 25-AUG-1999; 99US-00380139.

PR 25-AUG-1999; 99US-00380142.

PR 15-SEP-1999; 99US-00397342.

PR 18-OCT-1999; 99US-00403297.

PR 12-NOV-1999; 99US-00423844.

PR 30-DEC-1999; 99WO-US031274.

PR 18-FEB-2000; 2000WO-US004341.

PR 01-MAR-2000; 2000WO-US005601.

PR 02-MAR-2000; 2000WO-US005841.

PR 21-MAR-2000; 2000WO-US007532.

PR 22-MAY-2000; 2000WO-US014042.

PR 02-JUN-2000; 2000WO-US015264.

PR 22-AUG-2000; 2000US-00644848.

PR 24-AUG-2000; 2000WO-US023328.

PR 18-SEP-2000; 2000US-00654610.

PR 18-SEP-2000; 2000US-0065350.

PR 08-NOV-2000; 2000US-00709238.

PR 10-NOV-2000; 2000WO-US030873.

PR 01-DEC-2000; 2000WO-US032678.

PR 20-DEC-2000; 2000US-00747259.

PR 20-DEC-2000; 2000WO-US034956.

PR 28-FEB-2001; 2001WO-US006520.

PR 22-MAR-2001; 2001US-00816744.

PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 30-MAY-2001; 2001US-00870574.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 29-JUN-2001; 2001US-00869599.  
PR 18-JUL-2001; 2001US-00908827.  
PR 06-DEC-2001; 2001US-00068667.  
XX (GETH ) GENENTECH INC.  
XX  
PI Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
XX P-PSDB; ABU81221.  
DR WPI; 2003-341840/32.  
DR P-PSDB; ABU81221.  
XX  
PT New monoclonal antibody that binds to a secreted and transmembrane  
PT polypeptide, useful for detecting and purifying the polypeptide and also  
PT for treating conditions responsive to the antibody.  
XX  
PS Example 4; Fig 151; 235pp; English.  
XX  
CC The invention relates to an antibody that binds to a secreted and  
CC transmembrane polypeptide, PRO1136. The antibody is useful for preparing  
CC a medicament useful in the treatment of a condition responsive to anti-  
CC PRO antibody. The antibody is also useful in diagnostic assays for PRO,  
CC by detecting its expression in specific cells, tissues or serum, and for  
CC affinity purification of PRO from recombinant cell culture or natural  
CC sources. The present sequence represents a cDNA encoding a PRO  
CC polypeptide of the invention  
XX  
SQ Sequence 2598 BP; 687 A; 590 C; 648 G; 673 T; 0 U; 0 Other;

Query Match 98.1%; Score 2514.2; DB 8; Length 2598;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 2552; Conservative 0; Mismatches 8; Indels 3; Gaps 3;

Qy 1 AGGGGAGTCTACACCCCTGTGGAGCTCAAGATGGTCTCTAGTGGGGCGCTGTGTTCCGAA 60  
Db 38 AGGGGAGTCTACACCCCTGTGGAGCTCAAGATGGTCTCTAGTGGGGCGCTGTGTTCCGAA 97  
Qy 61 TGAAGACTCGGCATTGAAGTGTCTTATCTGCAATAAACCAGCTTCTAGCTGGAGGC 120  
Db 98 TGAAGACTCGGCATTGAAGTGTCTTATCTGCAATAAACCAGCTTCTAGCTGGAGGC 157  
Qy 121 TGCATGCGAGGAGGCTCATTAAAGTGAAGATCAGCGTGTCCCAATCGTGGCTCG 180  
Db 158 TGCATGCGAGGAGGCTCATTAAAGTGAAGATCAGCGTGTCCCAATCGTGGCTCG 217  
Qy 181 ATGCCAGCTGTCCCGGCTCATCTCTGGGTGTCCAGGTGGAAGCCAGTGCCTGTCTATGTG 240  
Db 218 ATGCCAGCTGTCCCGGCTCATCTCTGGGTGTCCAGGTGGAAGCCAGTGCCTGTCTATGTG 277  
Qy 241 GGGTGGGCGAGGCGGACTCTTAACACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG 300  
Db 278 GGGTGGGCGAGGCGGACTCTTAACACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG 337  
Qy 301 GTGCCAAGGAATCCAAGAGCTTCACTTCTACCGGGGAGACATGGGGCTCACTCCAGCT 360  
Db 338 GTGCCAAGGAATCCAAGAGCTTCACTTCTACCGGGGAGACATGGGGCTCACTCCAGCT 397  
Qy 361 TCGAGTTCGGCTGTCCCTACCGGGCTGTCTCTGTCAGCGTGTCTGAAGCCGATCAGCCTG 420  
Db 398 TCGAGTTCGGCTGTCCCTACCGGGCTGTCTCTGTCAGCGTGTCTGAAGCCGATCAGCCTG 457  
Qy 421 TCAGACTCACCCAGCTTCCCGAGATGGTGGTGAATGCCCCCATCACAGACTTCTACT 480  
Db 458 TCAGACTCACCCAGCTTCCCGAGATGGTGGTGAATGCCCCCATCACAGACTTCTACT 517  
Qy 481 TCCAGCAGTGTACTAGGGCAACGTGCCCCCCCCAGAACTCCCTGGGCGAGCAGCTCGG 540  
Db 518 TCCAGCAGTGTACTAGGGCAACGTG-CCCCCCAGAACTCCCTGGGCGAGCAGCTCGG 576

QY	541	GTGAGGGTGAGTGGAGGAGACCCATGGCGGACAATCACTCTTTCTGTCTCTCAGGACCCC	600
Db	577	GTGAGGGTGAGTGGAGGAGACCCATGGCGGACAATCACTCTCTGTCTCTCAGGACCCC	636
QY	601	CAGGTCGTAGTGTAGTGGGACCTGACCACTTTGTCTTCTGTGTCCAGTTTGCATAAATT	660
Db	637	CAGCTCTGACTAGTGGGACCTGACCACTTTGTCTTCTGTGTCCAGTTTGCATAAATT	696
QY	661	CTGAGATTGGGAGCTCAGTCCAGGGTCTCCGCCACTGGATGGTGCTACTGTGTGGAACT	720
Db	697	CTGAGATTGGGAGCTCAGTCCAGGGTCTCCGCCACTGGATGGTGCTACTGTGTGGAACT	756
QY	721	CTTTGTAATAACCATGTGGGGTAACTGGGAATAACATGAATAAATTTCTGTGGGGTGGG	780
Db	757	CTTTGTAATAACCATGTGGGGTAACTGGGAATAACATGAATAAATTTCTGTGGGGTGGG	816
QY	781	GTGGGGAGTGTGGGAATCATCTCTGCTTAATGGTAACTGACAAGTGTTCCTCTGAGCC	840
Db	817	GTGGGGAGTGTGGGAATCATCTCTGCTTAATGGTAACTGACAAGTGTTCCTCTGAGCC	876
QY	841	CGCAGGCCAACCCATCCCGAGTTGAGCCTTATAGGGTCAGTAGCTCTCCACATGAAGTC	900
Db	877	CGCAGGCCAACCCATCCCGAGTTGAGCCTTATAGGGTCAGTAGCTCTCCACATGAAGTC	936
QY	901	CTCTCACTCACCACCTGTGCAGGAGAGGGAGGTGGTCATAGAGTCAGGGATCTATGGCCCT	960
Db	937	CTGTCACTCACCACCTGTGCAGGAGAGGGAGGTGGTCATAGAGTCAGGGATCTATGGCCCT	996
QY	961	TGCCCCAGCCCAACCCCTTCCCTTT-ATCTGCGCACTGTCATATGCTACCTTCTCTATC	1019
Db	997	TGCCCCAGCCCAACCCCTTCCCTTTAAATCCTGCCACTGTCTATGCTACCTTCTCTATC	1056
QY	1020	TCTTCCCTCATCATCTTGTGTGGGCATGAGAGAGTGGTGATGTCAGAGAATAATGTTGCG	1079
Db	1057	TCTTCCCTCATCATCTTGTGTGGGCATGAGAGAGTGGTGATGTCAGAGAATAATGTTGCG	1116
QY	1080	AGCTCAGAAGATAAAGATAGTGGGTATGCTGATCCTCTTTTAAAAACCCCAAGATACA	1139
Db	1117	AGCTCAGAAGATAAAGATAGTGGGTATGCTGATCCTCTTTTAAAAACCCCAAGATACA	1176
QY	1140	ATCAAAATCCAGATGCTGCTCTATTCGCATGAATAAGTCTCATGATATGAGAA	1199
Db	1177	ATCAAAATCCAGATGCTGCTCTATTCGCATGAATAAGTCTCATGATATGAGAA	1236
QY	1200	GACCTACTTACAAAGTGGCATATATTGCAATTTATTTTAAATTAAGATACCTATTATTA	1259
Db	1237	GACCTACTTACAAAGTGGCATATATTGCAATTTATTTTAAATTAAGATACCTATTATTA	1296
QY	1260	TATTTCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTTGACAAATGTCAGGGTGG	1319
Db	1297	TATTTCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTTGACAAATGTCAGGGTGG	1356
QY	1320	TGGCAGTATAGGTGATTTTCTTTTAAATTTCTGTTAAATTTATCTGTTATTTCTTAAATTTTC	1379
Db	1357	TGGCAGTATAGGTGATTTTCTTTTAAATTTCTGTTAAATTTATCTGTTATTTCTTAAATTTTC	1416
QY	1380	TACAAATGAAGATGAATTCCTTGTATATAAATAAGAAAGAAATTAATCTTGAGGTAAAGCA	1439
Db	1417	TACAAATGAAGATGAATTCCTTGTATATAAATAAGAAAGAAATTAATCTTGAGGTAAAGCA	1476
QY	1440	GAGCAGACATCATCTCTGATTTGCTCAGCCTCCAATTCGCCAGAGTAATAATCAAAATTGA	1499
Db	1477	GAGCAGACATCATCTCTGATTTGCTCAGCCTCCAATTCGCCAGAGTAATAATCAAAATTGA	1536
QY	1500	ATCGAGCTCTGTGCTCTGTGGTGTAGTAGTATGAGGAAACAGATCTCAGCAAGC	1559
Db	1537	ATCGAGCTCTGTGCTCTGTGGTGTAGTAGTATGAGGAAACAGATCTCAGCAAGC	1596
QY	1560	CAGTGAAGGAGGCTGTGCTGAGTTTGTGTGGCTGGAATCTCTGGGTGAAGAACTTAA	1619
Db	1597	CAGTGAAGGAGGCTGTGCTGAGTTTGTGTGGCTGGAATCTCTGGGTGAAGAACTTAA	1656

QY	1620	GAACAAAAATCATCTGGTAATTTCTTCTAGAAAGGATCACAGCCCTGGGATTCCAAGGC	1679
Db	1657	GAACAAAAATCATCTGGTAATTTCTTCTAGAAAGGATCACAGCCCTGGGATTCCAAGGC	1716
QY	1680	ATTGGATCCAGTCTCTAAAGAGGCTGTGTCTGAAATTTGTCTCCCTCCAAATTC	1739
Db	1717	ATTGGATCCAGTCTCTAAAGAGGCTGTGTCTGAAATTTGTCTCCCTCCAAATTC	1776
QY	1740	CATCTTTCTTGGAACTCTCAGTCTGTGAGTTTATTTGGAGATAAGGTCTCTGAGATGTAG	1799
Db	1777	CATCTTTCTTGGAACTCTCAGTCTGTGAGTTTATTTGGAGATAAGGTCTCTGAGATGTAG	1836
QY	1800	TTAGTTAAGACAGGTCTGCTGGATGAAGTGAAGTCTAAATTTCAATTAATGCTGTTTCC	1859
Db	1837	TTAGTTAAGACAGGTCTGCTGGATGAAGTGAAGTCTAAATTTCAATTAATGCTGTTTCC	1896
QY	1860	TTGTATGAAAGGAGGACACAGAGACAGAGGACGCGGGAAGACTATATGAAGATG	1919
Db	1897	TTGTATGAAAGGAGGACACAGAGACAGAGGACGCGGGAAGACTATATGAAGATG	1956
QY	1920	AAGGCAGAGATCGGAGTTTTCAGCCACAAGCTAAGAAACACCAAGGATTTGGCAACCA	1979
Db	1957	AAGGCAGAGATCGGAGTTTTCAGCCACAAGCTAAGAAACACCAAGGATTTGGCAACCA	2016
QY	1980	TCAGAGCTTGGAAAGGACCAAGAAATTTCTTCTAGAGGCTTTAGAGGATTAACGCG	2039
Db	2017	TCAGAGCTTGGAAAGGACCAAGAAATTTCTTCTAGAGGCTTTAGAGGATTAACGCG	2076
QY	2040	TCGTCTGAAACCTTAATCTCAGACTTCCAGCTCTGAAACGAAGAAATAAATTTCCG	2099
Db	2077	TCGTCTGAAACCTTAATCTCAGACTTCCAGCTCTGAAACGAAGAAATAAATTTCCG	2136
QY	2100	CTGTTTAAAGCCACCAAGGATAAATTTGTACAGAGCTCTAGGAACTAATAACAGTGT	2159
Db	2137	CTGTTTAAAGCCACCAAGGATAAATTTGTACAGAGCTCTAGGAACTAATAACAGTGT	2196
QY	2160	AAAAATGATCCCTGCTCTCTGTTTACATTTCTGTGTGTCTCCCTCCCAACATGTACCA	2219
Db	2197	AAAAATGATCCCTGCTCTCTGTTTACATTTCTGTGTGTCTCCCTCCCAACATGTACCA	2256
QY	2220	AAATTTGCTTTCTGACCCCAATAGAAATATGGCAGAAAGTATGGCATGCCACTTCCAAGATT	2279
Db	2257	AAATTTGCTTTCTGACCCCAATAGAAATATGGCAGAAAGTATGGCATGCCACTTCCAAGATT	2315
QY	2280	AGGTTATAAAGACACTGCAGCTTCTACTTGTAGCCCTCTCTCTGTGCCACCCACCGCCCC	2339
Db	2316	AGGTTATAAAGACACTGCAGCTTCTACTTGTAGCCCTCTCTCTGTGCCACCCACCGCCCC	2375
QY	2340	CAATCTATCTTGGCTCACTGCTCTGGGGAGGCTAGCTGCCATGCTATGAGCAGCCCTA	2399
Db	2376	CAATCTATCTTGGCTCACTGCTCTGGGGAGGCTAGCTGCCATGCTATGAGCAGCCCTA	2435
QY	2400	TAAAGAGACTTACGTGGTAAATAAATAAGTCTCCCTGCCACAGCCACATTAAGTAACTTA	2459
Db	2436	TAAAGAGACTTACGTGGTAAATAAATAAGTCTCCCTGCCACAGCCACATTAAGTAACTTA	2495
QY	2460	GAAGCAGAGACTCTCTGTGAGATAATCGATTTTGTGTTTAAAGTTGCTCAGTTTGGTCT	2519
Db	2496	GAAGCAGAGACTCTCTGTGAGATAATCGATTTTGTGTTTAAAGTTGCTCAGTTTGGTCT	2555
QY	2520	AACTTTGTTATGAGCAATAGATAAATAATATATCCAGAGAAAGAG	2562
Db	2556	AACTTTGTTATGAGCAATAGATAAATAATATATCCAGAGAAAGAG	2598

RESULT 15

ACH66319

ID ACH66319 standard; cDNA; 2598 BP.

XX ACH66319;

XX AC

XX DT 14-OCT-2003 (first entry)

XX

DE Novel human secreted and transmembrane protein PRO4342 cDNA.

KW Human; secreted and transmembrane protein; PRO; gene; ss.

XX Homo sapiens.

XX US2003027986-A1.

XX 06-FEB-2003.

XX 02-MAY-2002; 2002US-00063549.

XX 30-DEC-1998; 98KR-00062142.

XX 08-MAR-1999; 99WO-US005028.

XX 14-MAY-1999; 99US-00311832.

XX 14-MAY-1999; 99WO-US010733.

XX 25-AUG-1999; 99US-00380137.

XX 25-AUG-1999; 99US-00380138.

XX 25-AUG-1999; 99US-00380139.

XX 25-AUG-1999; 99US-00380142.

XX 15-SEP-1999; 99US-00397342.

XX 18-OCT-1999; 99US-00403297.

XX 12-NOV-1999; 99US-00423844.

XX 30-DEC-1999; 99WO-US031274.

XX 18-FEB-2000; 2000WO-US004341.

XX 01-MAR-2000; 2000WO-US005601.

XX 02-MAR-2000; 2000WO-US005841.

XX 21-MAR-2000; 2000WO-US007532.

XX 22-MAY-2000; 2000WO-US014042.

XX 02-JUN-2000; 2000WO-US015264.

XX 22-AUG-2000; 2000US-00644848.

XX 24-AUG-2000; 2000WO-US023328.

XX 18-SEP-2000; 2000US-00664610.

XX 18-SEP-2000; 2000US-00665350.

XX 08-NOV-2000; 2000US-00709238.

XX 01-DEC-2000; 2000WO-US030873.

XX 20-DEC-2000; 2000US-00747259.

XX 20-DEC-2000; 2000WO-US034956.

XX 28-FEB-2001; 2001WO-US006520.

XX 22-MAR-2001; 2001US-00816744.

XX 10-MAY-2001; 2001US-00854208.

XX 10-MAY-2001; 2001US-00854280.

XX 30-MAY-2001; 2001US-00870574.

XX 01-JUN-2001; 2001WO-US017800.

XX 05-JUN-2001; 2001US-00874503.

XX 29-JUN-2001; 2001US-00869599.

XX 18-JUL-2001; 2001US-00908827.

XX 06-DEC-2001; 2001US-00006867.

XX (GETH ) GENENTECH INC.

XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;

XX Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

XX WPI; 2003-456358/43.

XX P-PSDB; ABO53335.

XX PRO polypeptide, useful for preparing a medicament for treating a

XX condition associated with PRO polypeptide.

XX Disclosure; Fig 151; 222pp; English.

XX The invention describes an isolated polypeptide having at least 80, 85,

XX 90, 95 or 99% identity with: (a) a sequence having 46-335 amino acids, or

XX its extracellular domain; (b) a sequence having 46-335 amino acids,

XX lacking its associated signal peptide; or (c) an amino acid sequence

XX encoded by the full-length coding sequence of the cDNA (ATCC accession

XX number 209956). The PRO (secreted and transmembrane) polypeptide is

XX useful for preparing a medicament for treating a condition associated

XX with PRO polypeptide. This sequence encodes a novel human secreted and

XX transmembrane PRO polypeptide

SQ	Sequence	2598 BP; 687 A; 590 C; 648 G; 673 T; 0 U; 0 Other;
Query Match	98.1%;	Score 2514.2; DB 8; Length 2598;
Best Local Similarity	99.6%;	Pred. No. 0;
Matches 2552; Conservative	0;	Mismatches 8; Indels 3; Gaps 3;
QY	1	AGGGAGTCTACACCTGTGGAGCTCAAGATGGTCTCTGAGTGGGGCGCTGTCTCCGAA 60
DB	38	AGGGAGTCTACACCTGTGGAGCTCAAGATGGTCTCTGAGTGGGGCGCTGTCTCCGAA 97
QY	61	TGAAGGACTCGGCATTGAAGTGTCTTATCTGCATAATAACCAAGCTTCTAGCTGGAGGC 120
DB	98	TGAAGGACTCGGCATTGAAGTGTCTTATCTGCATAATAACCAAGCTTCTAGCTGGAGGC 157
QY	121	TGCATGCAGGGAAGGTCAATAAGGTGAAGAGATCAGCGTGTGCCCAATCGTGGCTGG 180
DB	158	TGCATGCAGGGAAGGTCAATAAGGTGAAGAGATCAGCGTGTGCCCAATCGTGGCTGG 217
QY	181	ATGCCAGCTGTCCCGCTCATCTCGGTGTCCAGGTGGAAGCCAGTGCCTGTCTATGTG 240
DB	218	ATGCCAGCTGTCCCGCTCATCTCGGTGTCCAGGTGGAAGCCAGTGCCTGTCTATGTG 277
QY	241	GGGTGGGCGAGGAGCCGACTCTAACAATAGAGCCAGTGAACATCATGGAGCTCTATCTTG 300
DB	278	GGGTGGGCGAGGAGCCGACTCTAACAATAGAGCCAGTGAACATCATGGAGCTCTATCTTG 337
QY	301	GTGCCAAGAAATCCAAAGAGCTTCACTTCTACCGCGGGAATGAGGCTCACTCCAGCT 360
DB	338	GTGCCAAGAAATCCAAAGAGCTTCACTTCTACCGCGGGAATGAGGCTCACTCCAGCT 397
QY	361	TCGAGTGGCTGCTACCGGGCTGTTCTGTGACCGTGTGAGCGGATCAGCCGATCAGCCTG 420
DB	398	TCGAGTGGCTGCTACCGGGCTGTTCTGTGACCGTGTGAGCGGATCAGCCGATCAGCCTG 457
QY	421	TCAGACTCAACCAGCTTCCCGAGAAATGGTGGTGGAAATGCCCCCAATCAAGACTTCTACT 480
DB	458	TCAGACTCAACCAGCTTCCCGAGAAATGGTGGTGGAAATGCCCCCAATCAAGACTTCTACT 517
QY	481	TCCAGCAGTGTGACTAGGGCAACGTGCCCGGCAAGAACTCTCTGCTCTCAGGACCCC 540
DB	518	TCCAGCAGTGTGACTAGGGCAACGTG-CCCCCAGAACTCTCTGCTCTCAGGACCCC 576
QY	541	GTGAGGGGTGAGTGAGGAGACCCATGGCGGGAATCACTCTTCTGCTCTCAGGACCCC 600
DB	577	GTGAGGGGTGAGTGAGGAGACCCATGGCGGGAATCACTCTCTCTCTCAGGACCCC 636
QY	601	CAGGTCTGACTTGTAGTGGGCACCTGACCACTTGTCTCTGTTTCCAGTTTGCATAAAT 660
DB	637	CAGGTCTGACTTGTAGTGGGCACCTGACCACTTGTCTCTGTTTCCAGTTTGCATAAAT 696
QY	661	CTGAGATTGGAGCTCAGTCCAGGTCTCTCCCGGATGGATGGTGTCTGTGTGGAAC 720
DB	697	CTGAGATTGGAGCTCAGTCCAGGTCTCTCCCGGATGGATGGTGTCTGTGTGGAAC 756
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DB	757	CTTGTAAAAACCATGTGGGTAAACTGGGAATAACATGAAAGATTCTCTGGGGGTGG 816
QY	781	GTGGGGGAGTGTGGGAATCATTTCTGCTTAATGTTAACTGACAAAGTTTACCTCAGCC 840
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QY	841	CCGACGGGCAACCCATCCCGAGTTGAGCTTATAGGGTCAAGTGTCTCCACATGAAGTC 900
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QY	901	CTCTCACTCAACCATGTGTGAGGAGGAGGTGGTGTGATAGATCAGGATCTATGGCCCT 960
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DB	997	TGGCCCCCGCCACCCCTTCCCTTTAATCTTCCACTGTCTATGTCTACCTTTCTCTATC 1056



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QY	1080	AGCTCAGAAGATAAAGATAGGTAGGTATGCTGATCTCTTTTAAAAACCCGAAGATACA	1139
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QY	1260	TATTTCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTGTAGCAATGTCAGGGTGG	1319
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QY	1380	TACAAATGAAGATGAATTCCTTGTATAAAAATAAGAAAAAGAAATTAATCTTGAGGTAAACA	1439
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DB	1777	CATCCTTTCTGGAAATCTCAGTCTGTGAGTTTATTTGGAGATAAGGCTCTCTGCAGATGTAG	1836
QY	1800	TTAGTTAAGACAAGGTCTCATCTGATCAAGTAGACCTTAAATTCATATCAGCTGGTTTCC	1859
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QY	1980	TCAGAACTTGGAAAGGCAAGAAAGAAATTTCTTCCCTAGAGGCTTTTAGAGGGGATAACGGC	2039
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Qy	2100	CTGTTTAAAGCCCAAGAGTAATTTGGTTACAGCAGCTCTAGAGAACTAATACAGCTGCT	2159
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Job time : 1423.49 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 13, 2005, 11:56:15 ; Search time 8384.03 Seconds  
(without alignments)  
11636.250 Million cell updates/sec

Title: US-09-617-720A-1

Perfect score: 2563

Sequence: 1 agggaggtctacacctgtg.....ataatgcagagaagaaga 2563

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hic:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gss1:\*

9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2469.2	96.3	2605	3	CR613851 full-leng
2	1568.4	61.2	1648	3	BC000945 Homo sapi
3	980.2	38.2	1140	1	AL570964 AL570964
4	731.6	28.5	1080	7	CK232552 ILLUMIGEN
5	712.6	27.8	985	1	AL545100 AL545100
6	707.7	27.6	750	5	BX091500 BX091500
7	683.8	26.7	726	4	BI089828 602855071
8	656.2	25.6	876	5	BX350082 BX350082
9	644.6	25.2	702	6	CA310393 UI-H-F11-
10	643.2	25.1	697	2	BF509095 UI-H-B14-
11	631.6	24.6	858	4	BI090567 602855674
12	551.4	21.5	915	5	BX350083 BX350083
13	527.8	20.6	555	1	AUI38695 AUI38695
14	481.2	18.8	555	5	BQ351235 RCO-HT077
15	468.8	18.3	468	9	AY413262 Homo sapi
16	467.8	18.2	632	7	CV029389 8151 Full
17	465.8	18.1	467	8	AZ521126 RPI1-11-1
18	463.2	18.1	468	9	AY413263 Pan trogl
19	451.2	17.6	485	1	AIO40890 ow26a12.x
20	436.8	17.0	464	2	BF435174 nab43h02.
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24	393.6	15.4	435	2	BE711845 QV2-HT069

C	25	387.4	15.1	410	1	AI167887	0291C09.x
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	28	380.8	14.9	416	1	AUI57708	AUI57708
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	30	379.4	14.8	2841	3	AK014576	Mus muscu
C	31	373.4	14.6	885	6	CB589411	AGENCOURT
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	35	349.6	13.6	400	4	BG010066	PM4-GN030
	36	349.4	13.6	374	7	R70041	R70041.y148g04.s1
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	38	315.4	12.3	348	7	R70089	R70089.y148g04.r1
	39	300.4	11.7	338	5	BX477358	DKFZp6860
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	44	222.4	8.7	235	2	AW014217	UI-H-B10-
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#### ALIGNMENTS

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DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REMARK  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
ORIGIN  
Query Match  
Best Local Similarity  
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1 AGGGAGTCTACACCTGTGGAGCTCAAGATGGTCTGAGTGGGGCGCTGCTCCGAA 60  
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CR613851 2605 bp mRNA linear HTC 21-JUL-2004  
full-length cDNA clone CS0D1013YA07 of Placentia Cot 25-normalized  
of Homo sapiens (human).  
CR613851  
CR613851.1 GI:50494658  
HTC; CNSLT CDNA.  
Homo sapiens (human)  
Homo sapiens  
Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished  
Contact: Feng Liang Email: fliang@lifetech.com URL:  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Paraday Avenue  
2 (bases 1 to 2605)  
Genoscope.  
Direct Submission  
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)  
- Web : www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
Location/Qualifiers  
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/tissue type="placentia Cot 25-normalized"  
/plasmid="pCMVSPORT\_6"  
ORIGIN  
Query Match 96.3%; Score 2469.2; DB 3; Length 2605;  
Best Local Similarity 99.2%; Pred. No. 0;  
Matches 2513; Conservative 0; Mismatches 18; Indels 3; Gaps 3;  
1 AGGGAGTCTACACCTGTGGAGCTCAAGATGGTCTGAGTGGGGCGCTGCTCCGAA 60  
74 AGGGAGTCTACACCTGTGGAGCTCAAGATGGTCTGAGTGGGGCGCTGCTCCGAA 133



QY 61 TGAAGGACTCGGCAATGAAGGTGCTTTATCTGCATATAAACAAGCTTCTAGCTGGAGGC 120  
DB 134 TGAAGGACTCGGCAATGAAGGTGCTTTATCTGCATATAAACAAGCTTCTAGCTGGAGGC 193  
QY 121 TGCATCGAGGGAAGGTCAATTAAGGTGAAGAGATCAGCGTGTGCCAATCCGCTGGCTGG 180  
DB 194 TGCATCGAGGGAAGGTCAATTAAGGTGAAGAGATCAGCGTGTGCCAATCCGCTGGCTGG 253  
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DB 314 GGTGGGGCAGGAGCGAGCTCTAACAAGGTGAAGAGATCAGCGTGTGCCAATCCGCTGG 373  
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Db      2592 AACTTGTATTGAG 2605

```

## RESULT 2

```

BC000945
LOCUS      BC000945      1648 bp      mRNA      linear      HTC 19-NOV-2003
DEFINITION Homo sapiens interleukin 1 family, member 5 (delta), mRNA (CDNA
clone IMAGE:3447369), with apparent retained intron.

```

```

ACCESSION BC000945.2 GI:14705316

```

## KEYWORDS

```

SOURCE      HTC.

```

```

ORGANISM    Homo sapiens (human)

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

1 (bases 1 to 1648)

```

```

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farnet,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullaby,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahy,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalls,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
2338257
12477932
2 (bases 1 to 1648)
Strausberg,R.
Direct Submission
Submitted (16-NOV-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgi.nci.nih.gov
On Jul 12, 2001 this sequence version replaced gi:13937574.
Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.

```

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REMARK

## COMMENT

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome  
Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulsegod, H.,

Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,

A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 3 Row: 1 Column: 18

This clone has the following problem: retained intron.

Location/Qualifiers

1. 1648

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/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3447369"

/tissue\_type="Placenta, choriocarcinoma"

/clone\_lib="NIH MGC\_10"

/lab\_host="DH10B"

/note="Vector: pCMV-SPORT6"

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QY 1674 CAAGGCATTGGATCCAGTCTCTAAGAAGGCTCTGTACTGTGGTGAATTTGTGCCCCCTCA 1733
Db 721 CAAGGCATTGGATCCAGTCTCTAAGAAGGCTCTGTACTGTGGTGAATTTGTGCCCCCTCA 780
QY 1734 AATTCATCCTCTTGGAAATCTCAGTCTGTGAGTTTATTTGGAGATAAGGTTCTCTGAG 1793
Db 781 AATTCATCCTCTTGGAAATCTCAGTCTGTGAGTTTATTTGGAGATAAGGTTCTCTGAG 840
QY 1794 ATGTAGTCTAGTTAAGACAGGTCATCTCGATGAAGGTAGACTTAATTTCAATATGACTG 1853
Db 841 ATGTAGTCTAGTTAAGACAGGTCATCTCGATGAAGGTAGACTTAATTTCAATATGACTG 900
QY 1854 GTTTCCTCTGTATGAAAGGAGAGGACACAGAGACAGAGAGAGCGGGGAAAGACTATGTA 1913
Db 901 GTTTCCTCTGTATGAAAGGAGAGGACACAGAGACAGAGAGAGCGGGGAAAGACTATGTA 960
QY 1914 AAGATGAAGCAGAGATCGAGTTTTCAGGCTTTCCTAGAGGCTTTAGAGGGAT 2033
Db 961 AAGATGAAGCAGAGATCGAGTTTTCAGGCTTTCCTAGAGGCTTTAGAGGGAT 1020
QY 1974 CAACCATCAGAGCTTGGAAAGGAGGCAAGAAATTTCTTCTAGAGGCTTTAGAGGGAT 2033
Db 1021 CAACCATCAGAGCTTGGAAAGGAGGCAAGAAATTTCTTCTAGAGGCTTTAGAGGGAT 1080
QY 2034 AAGCGGTCTGCTGAAACCTTAAATCTCAGACTTCCAGCCTCTGAAAGAAAGAAATAAA 2093
Db 1081 AAGCGGTCTGCTGAAACCTTAAATCTCAGACTTCCAGCCTCTGAAAGAAAGAAATAAA 1140
QY 2094 TTTCCGCTGTTTAAAGCCCAAGGATAATTTGGTTACAGAGCTCTAGAAACTAATACA 2153
Db 1141 TTTCCGCTGTTTAAAGCCCAAGGATAATTTGGTTACAGAGCTCTAGAAACTAATACA 1200
QY 2154 GCTGCTAAATGATCCCTGCTCTCTGTTTACATTTCTGTGTGCTGCTCCCTCCCAAT 2213
Db 1201 GCTGCTAAATGATCCCTGCTCTCTGTTTACATTTCTGTGTGCTGCTCCCTCCCAAT 1260
QY 2214 GTACCAAGTGTCTTTGTGACCCCAATAGAAATAGGAGAGTGTGAGTGCACCTTC 2273
Db 1261 GTACCAAGTGTCTTTGTGACCCCAATAGAAATAGGAGAGTGTGAGTGCACCTTC 1319
QY 2274 AAGATAGGTTATAAAGACACTGCAGCTTCTACTTGAGCCCTCTCTCTGCCCCAC 2333
Db 1320 AAGATAGGTTATAAAGACACTGCAGCTTCTACTTGAGCCCTCTCTCTGCCCCAC 1379
QY 2334 CGCCCCCAATCTATTTGGCTCACTCGCTCTGGGGGAAGCTAGCTGCATGCTATGACA 2393
Db 1380 CGCCCCCAATCTATTTGGCTCACTCGCTCTGGGGGAAGCTAGCTGCATGCTATGACA 1439
QY 2394 GGCTATAAAGAGACTTACGTGGTAAATAATGAAGTCTCTGCCCCACAGCCACATTAGT 2453
Db 1440 GGCTATAAAGAGACTTACGTGGTAAATAATGAAGTCTCTGCCCCACAGCCACATTAGT 1499
QY 2454 AACCTAGAGCAGAGACTCTGTGAGATAATCGATTTGTTGTTTAAAGTTGCTCAGTTT 2513
Db 1500 AACCTAGAGCAGAGACTCTGTGAGATAATCGATTTGTTGTTTAAAGTTGCTCAGTTT 1559
QY 2514 TGGTCTAACTTGTATGAGCAATAGATAAATATATATGAGAGAAAGAGA 2563
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RESULT 3
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LOCUS AL570964 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1013YA07 3-PRIME, mRNA sequence.
ACCESSION AL570964
VERSION AL570964.3 GI:46237085
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EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1. (bases 1 to 1140)  
Li, W.B., Gruber, C., Jesse, J., and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
On Feb 16, 2001 this sequence version replaced gi:31292372.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
1383.f  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?s=CS0D1013AA04NP1&c=1383.f.  
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/db\_xref="taxon:9606"  
/clone="CS0D1013YA07"  
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/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

Query Match 38.2%; Score 980.2; DB 1; Length 1140;  
Best Local Similarity 98.9%; Pred. No. 3.2e-242; Indels 2; Gaps 2;  
Matches 1004; Conservative 3; Mismatches 6;

QY 1519 GTTGGTGTGTAGTAGATCAGGAACAGATCTCAGCAAGCCACTGAGGAGGCTGTG 1578  
Db 1013 GXTKGTGTGTAGTAGATCA-GAAACAGATCTCAGCAAGCCACTGAGGAGGCTGTG 955  
QY 1579 CTGAGTTGTGTGGTGAATCTCTGGGTAGGAATCTTAAAGAACAAAATCATCTGTA 1638  
Db 954 ATGAGTTGTGTGGTGAATCTCTGGGTAGGAATCTTAAAGAACAAAATCATCTGTA 895  
QY 1639 ATTCTTCTAGAGGATCAGAGCCCTGGGATTCAGAGGATTCAGTCTCTAAG 1698  
Db 894 ATTCTTCTAGAGGATCAGAGCCCTGGGATTCAGAGGATTCAGTCTCTAAG 835  
QY 1699 AAGGCTGTGTACTGTGTAATTTGTGCTCCCTCAAAATTCACATCTTCTTGAATCTCA 1758  
Db 834 AAGGCTGTGTACTGTGTAATTTGTGCTCCCTCAAAATTCACATCTTCTTGAATCTCA 775  
QY 1759 GTCTGTGATTTATTTGGAGATAAGCTCTCTCCAGATGTAGTCTAAGCAAGTCTAT 1818  
Db 774 GTCTGTGATTTATTTGGAGATAAGCTCTCTCCAGATGTAGTCTAAGCAAGTCTAT 715  
QY 1819 GCTGGATGAAGGTAGACCTTAAATTCATATGACTGGTTTCTTGTATGAAAGGAGAGA 1878  
Db 714 GCTGGATGAAGGTAGACCTTAAATTCATATGACTGGTTTCTTGTATGAAAGGAGAGA 655  
QY 1879 CACAGAGACAGAGGAGAGCGGGGAGAGACTATGTAAAGATGAAGGAGAGATCGGATTT 1938  
Db 654 CACAGAGACAGAGGAGAGCGGGGAGAGACTATGTAAAGATGAAGGAGAGATCGGATTT 595  
QY 1939 TGCAGCCACAGCTAAGAAACACCCAGGATTTGGCAACCATCAGAGCTTGGAGAGAGC 1998  
Db 594 TGCAGCCACAGCTAAGAAACACCCAGGATTTGGCAACCATCAGAGCTTGGAGAGAGC 535  
QY 1999 AAAGAAGAATTTCTTCCCTAGAGGCTTTAGAGGGGATAACGGCTCTGCTGAAACCTTAATCT 2058

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|||||
Db 534 AAAGAGAATCTTCCCTAGAGGCTTTAGAGGATAACGGCTCTGCTGAACCTTAATCT 475
QY 2059 CAGACTTCAGGCTCTCTGAACGAAGAAAGATAAATTTTCGGCTGTTTAAAGCCACCAAGG 2118
Db 474 CAGACTTCAGGCTCTCTGAACGAAGAAAGATAAATTTTCGGCTGTTTAAAGCCACCAAGG 415
QY 2119 ATAATTTGGTTACAGAGCTCTAGGAACTAATAACAGCTGCTAAATGATCCCTGCTCT 2178
Db 414 ATAATTTGGTTATGGCAGCTCTAGGAACTAATAACAGCTGCTAAATGATCCCTGCTCT 355
QY 2179 CGTGTTCATCTGTGTGTGTCCTCCCAATGTACCAATGTACCAATGTCTTTGTGACCA 2238
Db 354 CGTGTTCATCTGTGTGTGTCCTCCCAATGTACCAATGTACCAATGTCTTTGTGACCA 296
QY 2239 ATAGAATATGGCAGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 2298
Db 295 ATAGAATATGGCAGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 236
QY 2299 AGCTTCTACTGAGGCTCTCTCTCTGCGCCACACCGCCGCCCAATCTATCTTGGCTCACT 2358
Db 235 AGCTTCTACTGAGGCTCTCTCTCTGCGCCACACCGCCGCCCAATCTATCTTGGCTCACT 176
QY 2359 CGCTCTGGGGAGCTAGCTGCTGCTATGAGCAGGCTTATAAGAGACTTACGTGTA 2418
Db 175 CGCTCTGGGGAGCTAGCTTCCATGCTATGAGCAGGCTTATAAGAGACTTATGTGTA 116
QY 2419 AAAATGAAGTCTCTGCGCCACACGACATTTAGTGAACCTTAGAAGCAGAGACTCTGTGAG 2478
Db 115 AAAATGAAGTCTCTGCGCCACACGACATTTAGTGAACCTTAGAAGCAGAGACTCTGTGAG 56
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RESULT 4
CK232552
LOCUS
DEFINITION
  CK232552 1080 bp mRNA linear EST 09-DEC-2003
  ILLUMIGEN_MCO_4234 Katze MMLP2 Macaca mulatta cDNA 5' similar to
  human IL1F5 (Hs.207224), mRNA sequence.
ACCESSION
  CK232552
VERSION
  EST.
KEYWORDS
  Macaca mulatta (rhesus monkey)
SOURCE
  Macaca mulatta
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
  Cercopithecoidea; Macaca.
REFERENCE
  Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L.
  Large-scale Rhesus Macaque cDNA Sequencing
  Unpublished (2003)
  Contact: C. Magness
  Illumigen Biosciences Inc.
  2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
  Tel: 2063780400
  Fax: 2063780408
  Email: cmagness@illumigen.com
  Sequenced on 2003.12.02. 777 Q20 bases. Assemblies in contig w/ 1
  member(s). Contig contains 1 (0%) lib members.
PCR PRIMERS
  FORWARD: CCCTCACTAAAGGGAACAAA
  BACKWARD: CACTATAGGGCGAATGGGTA
  Insert Length: 1080 Std Error: 0.00
  Plate: CL000050 row: B column: 10
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1; Site: 2: Xho I; Created from Stratagene ZAP-CDNA
Synthesis kit (catalog #200400) and ZAP-CDNA Gigapack III
Gold Cloning Kit (Catalog #200450)"
ORIGIN
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Best Local Similarity 89.6%; Pred. No. 7.8e-178;
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QY 1400 TGTATAAATAAGAAAAGAAATTAATCTTGAAGTAAAGCAGAGACATCATCTCTGAT 1459
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Db 121 TGCCTCTCAGCTTCCCAATTTCCCAAGAGTTAAATTTCAAACTGAATTTGAGCTCTGCTGCTCTG 180
QY 1519 GTTGGTTGTAGTAGTATCAGGAAACAGATCTCAGCAAAAGCCACTCAGGAGGAGGCTGTG 1578
Db 181 GTTGGTTGTAGTAGTATCAGGAAACAGATCTCAGCAAAAGCCACTCAGGAGGAGGCTGTG 240
QY 1579 CTGAGTTTGTGCTGGGAATCT-CTGGGTAAAGGAACCTTAAAGAAACAAATCATCTGCT 1637
Db 241 ATGAGTTTGTGCTGGGAATCTCTCTGGGTAAAGGAACCTTAAAGAAACAAATCATCTGCT 300
QY 1638 AATTC-TTTCCTAGAGGATCAGCCCTCGGATTCGAAGGATTCGATTCAGTCTCTA 1696
Db 301 AATTCCTTCTAGAGGATCAGCCCTCGGATTCGAAGGATTCGATTCAGTCTCTA 360
QY 1697 AGAAGGCTGCTCTACTGTTGATTTGTGTCCTCAAAATTCACATCTCTTTTGAATCT 1756
Db 361 AGAAGGCTGCTCTACTGTTGATTTGTGTCCTCAAAATTCACATCTCTTTTGAATCT 420
QY 1757 CAGTCTGTGAGTTTATTTGGAGATAAGGCTCTCTGAGATGTAGTTAGTTAAGCAAGGTC 1816
Db 421 CGGCTCTGAGCTTATTTGGAGATAAGGCTCTCTGAGATGTAGTTAGTTAAGCAAGGTC 480
QY 1817 ATGCTGGATGAAGGTAGACCTAAATTTCAATATGACTGTTTCTTGTATGAAGAGAGAG 1876
Db 481 ATGCTGGATGAAGGTAAACCTTAAATTTCAATATGACTGTTTCTTGTATGAAGAGAGAG 540
QY 1877 GACACAGAGACA- ---GAGGAGACGCGGGGAAGACTATGTAAGATGAAGCAGAGATC 1931
Db 541 GACACAGAGACAAGAGGATGCGGGGAAGACTATGTAAGATGAAGCAGAGATGATA 600
QY 1932 GGAGTTTTCAGCCACAGCTAAGAAACACCAAGGATTTGCGCAACCATCAGAGGCTTG 1991
Db 601 GGAGTTGTCGCGCCACAGCCCAAGCAACCAAGGATTTGCGCAACCATCAGAGGCTTG 660
QY 1992 AAGAGGCAAGAGAAATTTCTTCCCTAGAGGCTTTTGAAGGATTAACGGCTCTGCTGAAC 2051
Db 661 AAGAGGCAAGAGAAATTTCTTCCCTAGAGGCTTTTGAAGGATTAACGGCTCTGCTGAAC 720
QY 2052 TTAATCTCAGACTTCCAGCTCTGAAAGCAAGAAATAAATTTTCGGCTGTTTAAAGCC 2111
Db 721 TTAATCTCAGACTTCTAGCTTCTGAAAGCAAGAAATAAATTTTCGACTGTTTAAAGCC 780
QY 2112 ACCAAGGATTAATTTGTTTACAGAGCTCTAGGAAACCTAATACAGCTGCTAAAATGATCCCT 2171
Db 781 ACCAAGGATTAATTTGTTTGGAGCTCTGAAAGCAAGAAATAAATTTTCGACTGTTTAAAGCC 840
QY 2172 GTCTCTCGTGTATTAATTTCTGTTGTCCTCCCAATGTACCAAGTGTGCTTTG 2231
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QY      2232  TGACCAATAGATATATGCGAAGTGTATGG 2261
Db      901  TGACTAATAAATAATGCCAAAGTGTATGG 930

RESULT 5
AL545100
LOCUS      985 bp      mRNA      linear      EST 25-MAR-2004
DEFINITION Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI013A07 5-PRIME, mRNA sequence.
ACCESSION  AL545100
VERSION      1
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 985)
AUTHORS    Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE      Full-length cDNA libraries and normalization
JOURNAL    Unpublished (2001)
COMMENT    On Feb 15, 2001 this sequence version replaced gi:31266936.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            1383.f
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CSODI013AA04QPl&c=1383.f.
FEATURES             source
    source
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            /db_xref="taxon:9606"
            /clone="CSODI013A07"
            /tissue_type="PLACENTA COT 25-NORMALIZED"
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            /notes="1st strand cDNA was primed with a NotI-oligo(dT)
            primer. Five prime end enriched, double-strand cDNA was
            digested with Not I and cloned into the Not I and EcoR V
            sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match      27.8%; Score 712.6; DB 1; Length 985;
Best Local Similarity 96.5%; Pred. No. 6.4e-173;
Matches 767; Conservative 4; Mismatches 18; Indels 6; Gaps 4;
QY      1  AGGGAGTCTACACCTGTGGAGCTCAAGATGCTCTGAGTGGGGCGCTGTGCTCCGAA 60
Db      74  AGGGAGTCTACACCTGTGGAGCTCAAGATGCTCTGAGTGGGGCGCTGTGCTCCGAA 133
QY      61  TGAAGACTCGGATTAAGAGTCTTATCTGCAATATACCAAGCTTCTAGCTGGAGGC 120
Db      134  TGAAGACTCGGATTAAGAGTCTTATCTGCAATATACCAAGCTTCTAGCTGGAGGC 193
QY      121  TGCATCGAGGAAGGTCATTAAAGGTGAAGAGATCAGCGTGGTCCCAATCGGTGGCTGG 180
Db      194  TGCATCGAGGAAGGTCATTAAAGGTGAAGAGATCAGCGTGGTCCCAATCGGTGGCTGG 253
QY      181  ATGCCAGCTGTCCCCCGTCATCTCTGGGTGTCAGGGTGAAGCCAGTGCCTGTATGTG 240
Db      254  ATGCCAGCTGTCCCCCGTCATCTCTGGGTGTCAGGGTGAAGCCAGTGCCTGTATGTG 313
QY      241  GGTGGGGGAGGAGCGACTCTAACACTAGACGACCTGACATCATGAGGAGCTCTATCTTG 300
Db      314  GGTGGGGGAGGAGCGGACTCTAACACTAGACGACCTGACATCATGAGGAGCTCTATCTTG 373
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QY      301  GTCCAAAGGAATCCAAAGCTTTCACCTTCTACCGCGGGACATGGGGTCTCACTCCAGCT 360
Db      374  GTGCCAAGGAATCCAAAGCTTTCACCTTCTACCGCGGGACATGGGGTCTCACTCCAGCT 433
QY      361  TCGAGTCCGCTGCCCTACCCGGGCTGGTTCCTGTGTGCACGGTGCTGAAGCCGATACGCTTG 420
Db      434  TCGAGTCCGCTGCCCTACCCGGGCTGGTTCCTGTGTGCACGGTGCTGAAGCCGATACGCTTG 493
QY      421  TCAGACTCACCCAGCTTCCCGAGATGTGGGTGGAAATGCCGCCATCACAGACTTCTACT 480
Db      494  TCAGACTCACCCAGCTTCCCGAGATGTGGGTGGAAATGCCGCCATCACAGACTTCTACT 553
QY      481  TCAGCAGTGTCTAGTAGGCAACGTGCCGCCCCAGAACTCCCTGGGCACAGCAGCTCGG 540
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QY      541  GTGAGGGGTGAGTGAGGAGAGACCCATGGCGGACAATCACTCTTTCTGTCTCAGACCCC 600
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QY      601  CAGGCTCAGCTTAGTGGGCACCTGACCACTTGTCTCTCTGTTCCAGTTTCGATATAATT 660
Db      673  CAGGCTCAGCTTAGTGGGCA-CTGACCACCTTTGTCTCTGTGTTCCAGTTTGGATAAAT 731
QY      661  CTGAGATTGGAGCTCAGTCCAGGGTCTCTCCCCCACTGGATGGTCTACTGTGTGGAA 720
Db      732  CTGAGATTGGAGCTCAGTCCAGGGTCTCTCCCCCACTGGATGGTCTACTGTGTGGAA 791
QY      721  CTTGTAATAAACCATGTGGGTAACTGGGAATACATGAAAGATTTCTGTGGGGTGGG 780
Db      792  CTTGT-AAAACCATGTGGGTAACTGGGATAMA---TGAAGAAGATTTCTGTGGGGTGGG 847
QY      781  GTGGGGGAGTGTCTGG 795
Db      848  GTGGGGGAGTGTGGG 862

RESULT 6
BX091500
LOCUS      750 bp      mRNA      linear      EST 23-JAN-2003
DEFINITION Homo sapiens placentae N2HP Homo sapiens cDNA clone
IMAGE:142518, mRNA sequence.
BX091500
ACCESSION  BX091500.1 GI:27822499
VERSION    BX091500.1
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 750)
AUTHORS    Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
            Radloff, U., Schneider, D. and Korn, B.
TITLE      Human Unigeneset - RZPD3
JOURNAL    Unpublished (2003)
COMMENT    Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
            RZPD; IMAGp998H07211.
            RZPDLib; I.M.A.G.E. cDNA Clone Collection;
            Human Unigeneset - RZPD3 (RZPDLib No.972)
            http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 101
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available royalty-free from RZPD;
            contact RZPD (clone@rzpd.de) for further information. Seq primer:
            M13r, Primer sequence: TTTCACAGGAACAGCTATGAC.
FEATURES             Location/Qualifiers
    source
        1..750
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/sex="Female"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares placenta Nb2HP"
/notes="Organ: placenta; Vector: pT73D (Pharmacia) with a
modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
AAGTGAAGAATTCCGGCGCCAGGAAATTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Patima Bernaldo. "
```

ORIGIN

Query Match 27.6%; Score 707; DB 5; Length 750;  
Best Local Similarity 99.3%; Pred. No. 1.7e-171;  
Matches 729; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 1830 GTAGACCTAAATTCATATGACTGGTTTCCTTGATGAAGAGGAGGACACAGACAG 1889  
DB 1 GTAGACCTAAATTCATATGACTGGTTTCCTTGATGAAGAGGAGGACACAGACAG 59  
QY 1890 AGGAGACGGGGGAGAGACTATGTAAGAGTGAAGGACAGATCGAGTTTTCGAGCCACAA 1949  
DB 60 AGGAGACGGGGGAGAGACTATGTAAGAGTGAAGGACAGATCGAGTTTTCGAGCCACAA 119  
QY 1950 GTTAAGAAACACCAAGGATGTGGCAACCATCAGAGCTTGGAAAGGCAAGAGAAT 2009  
DB 120 GCTAAGAAACACCAAGGATGTGGCAACCATCAGAGCTTGGAAAGGCAAGAGAAT 179  
QY 2010 CTTCCCTAGAGCTTTAGAGGATACGGCTGTGCTGAACCTTAATCTCAGACTTCCAG 2069  
DB 180 CTTCCCTAGAGCTTTAGAGGATACGGCTGTGCTGAACCTTAATCTCAGACTTCCAG 239  
QY 2070 CTTCCCTGAAGAGAAAGATAATTTTCGCTGTGTTTAAAGCCACCAAGGATATTCGTTA 2129  
DB 240 CTTCCCTGAAGAGAAAGATAATTTTCGCTGTGTTTAAAGCCACCAAGGATATTCGTTA 299  
QY 2130 CAGCAGCTCTAGGAACTAATACAGCTGTCTAAATGATCCCTGTCTCTCGTTTACAT 2189  
DB 300 CAGCAGCTCTAGGAACTAATACAGCTGTCTAAATGATCCCTGTCTCTCGTTTACAT 359  
QY 2190 TCTGTGTGTCCCTCCACAAATGACCAAGTTGCTTTGTGACCCCAATAGATATGG 2249  
DB 360 TCTGTGTGTCCCTCCACAAATGACCAAGTTGCTTTGTGACCCCAATAGATATGG 418  
QY 2250 CAGAAGTGTGCTATGCTCCAGATTTAGGTTATTAAGACACTGCGACTTCTACAT 2309  
DB 419 CAGAAGTGTGCTATGCTCCAGATTTAGGTTATTAAGACACTGCGACTTCTACAT 478  
QY 2310 GAGCCCTCTCTCTGCCACCCACCCGCCCAATCTATCTTGCTCACTCGCTCTGGGG 2369  
DB 479 GAGCCCTCTCTCTGCCACCCACCCGCCCAATCTATCTTGCTCACTCGCTCTGGGG 538  
QY 2370 AAGCTAGTGCCTATGATGAGCAGCGCTTATAAGAGACTTACGTGGTAAAAAATGAAT 2429  
DB 539 AAGCTAGTGCCTATGATGAGCAGCGCTTATAAGAGACTTACGTGGTAAAAAATGAAT 598  
QY 2430 CTTCCCTGCCACAGCCACATTTAGTGAACCTAGAGCAGAGACTCTGTGAGATATCGATGT 2489  
DB 599 CTTCCCTGCCACAGCCACATTTAGTGAACCTAGAGCAGAGACTCTGTGAGATATCGATGT 658  
QY 2490 TTGTTGTTTTAAAGTTGCTCAGTTTTTGGTCTAACTGTTATGACGCAATAGATAAATAA 2549  
DB 659 TTGTTGTTTTAAAGTTGCTCAGTTTTTGGTCTAACTGTTATGACGCAATAGATAAATAA 718  
QY 2550 TGCAGAGAAAGAGA 2563  
|||||

Db 719 TGCAGAGAAAGAGA 732

RESULT 7  
BI089828  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BI089828 726 bp mRNA linear EST 20-JUN-2001  
602855071F1 NIH\_MGC\_10 Homo sapiens cDNA clone IMAGE:4996432 5',  
mRNA sequence.  
BI089828  
BI089828.1 GI:14508158  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 726)  
NIH-MGC <http://mgi.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Incyte Genomics, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L14M11021 row: n column: 17  
High quality sequence stop: 709.

FEATURES  
Location/Qualifiers  
1..726  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4996432"  
/cell\_line="MGC36"  
/lab\_host="DH10B"  
/clone\_lib="NIH MGC 10"  
/note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.5 Kb. Library prepared by Life  
Technologies."

ORIGIN

Query Match 26.7%; Score 683.8; DB 4; Length 726;  
Best Local Similarity 98.1%; Pred. No. 1.7e-165;  
Matches 713; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

QY 40 GTGGGGCGCTGTGCTTCCGAATGAAGGACTCGGCATTGAAGGTGCTTTTATCTGCATAATA 99  
DB 1 GTGGGGCGCTGTGCTTCCGAATGAAGGACTCGGCATTGAAGGTGCTTTTATCTGCATAATA 60  
QY 100 ACCAGCTTCTAGCTGAGGGCTGCATGCGAGGAAGTCAATTAAGGTGAAGAGATCAGCG 159  
DB 61 ACCAGCTTCTAGCTGAGGGCTGCATGCGAGGAAGTCAATTAAGGTGAAGAGATCAGCG 120  
QY 160 TGGTCCCCCAATCGGTGGCTGGATGCCAGCTGTCCCCGTCTATCTGGGTGTCACGGGTG 219  
DB 121 TGGTCCCCCAATCGGTGGCTGGATGCCAGCTGTCCCCGTCTATCTGGGTGTCACGGGTG 180  
QY 220 GAAGCCAGTGCCTGTCTCATGTGGGGTGGGCGAGGAGCCGACTCTAACTAGAGCCAGTGA 279  
DB 181 GAAGCCAGTGCCTGTCTCATGTGGGGTGGGCGAGGAGCCGACTCTAACTAGAGCCAGTGA 240  
QY 280 ACATCATGAGCTCTATCTTTGTGTGCAAGGAATCCAAGAGCTTCACTTCTACCGGGGG 339  
DB 241 ACATCATGAGCTCTATCTTTGTGTGCAAGGAATCCAAGAGCTTCACTTCTACCGGGGG 300  
QY 340 ACATGGGGCTACCTCCAGCTTCCAGTCCGCTTACCCGGGCTGGTTCCTGTGACCG 399  
DB 301 ACATGGGGCTACCTCCAGCTTCCAGTCCGCTTACCCGGGCTGGTTCCTGTGACCG 360



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QY 400 TGCCTGAAGCCGATCAGCTGTGAGACTCACCAGCTTCCCGAGAAATGTCGCTGAATG 459
Db 361 TGCCTGAAGCCGATCAGCTGTGAGACTCACCAGCTTCCCGAGAAATGTCGCTGAATG 420
QY 460 CCCCATCACAGACTTCTACTTCCAGAGTGTGACTAGGCAACGTCGCCCCAGAACT 519
Db 421 CCCCATCACAGACTTCTACTTCCAGAGTGTGACTAGGCAACGTCGCCCCAGAACT 479
QY 520 CCTGGGAGAGCAGCTGGGTGAGGGTGTGAGTGGAGAGAGCCCATGGGACAACTCAC 579
Db 480 CCTGGGAGAGCAGCTGGGTGAGGGTGTGAGTGGAGAGAGCCCATGGGACAACTCAC 539
QY 580 TCTTCTGTCTCAGACCCCAAGTGTGACTTGTAGTGGGACCTGACCACTTGTCTTCT 639
Db 540 TCTTCTGTCTCAGGACCCCAAGTGTGACTTGTAGTGGGACCTGACCACTTGTCTTCT 599
QY 640 GGTTCAGGTTGCATAAATTCGAGATTGGAGCTCAGTCCAGGTCCT-CCCCACTG 698
Db 600 GGTTCAGGTTGCATAAATTCGAGATTGGAGCTCAGTCCAGGTCCTCAGCCCACTG 659
QY 699 GATGGTGTCTGTCTGTGAACCTTGTAAACCATGTGGGGTAAACTGGGATCACTG 758
Db 660 GATGGTGTCTGTCTGTGAACCTTGTAAACCATGTGGGGTAAACTGGGATCACTG 719
QY 759 AAAAGAT 765
Db 720 AAAAGAT 726
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```
RESULT 8
BX350082/c
LOCUS
DEFINITION
BX350082 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1013YA07 3-PRIME, mRNA sequence.
ACCESSION
BX350082
VERSION
BX350082.2 GI:46553560
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 876)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30383464.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
1383.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS08A1018ZD02_CS01644_1&c=1383.f
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FEATURES
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Location/Qualifiers
1..876
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1013YA07"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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ORIGIN

```
Query Match 25.6%; Score 656.2; DB 5; Length 876;
Best Local Similarity 90.4%; Pred. No. 2.5e-158;
Matches 779; Conservative 0; Mismatches 74; Indels 9; Gaps 7;

QY 759 AAAAGATTTCTGTGGGGTGGGGTGGGGAGTGTGGGAATCATTCCTGCTTAATGGTAA 818
Db 876 AAAATTTTCTTGGGGGTGGGGTGGGAAATAAGAGCAACATTCCTCCGGTTAAGGCCA 817
QY 819 CTGACAAGTGTTPACCC--TGAGCCCCCGAGGCAACCCATCCCTGTTGAGCCTT-ATAG 875
Db 816 CCGCCAAAGGGTCCCTTAAAGCCCGGGTTACCCCATCCCAAGTGAACCTTAATAG 757
QY 876 GGTGAGTGTCTCTCAC-ATGAAGTCTCTCACT-CAACACTGTGAGAGAGGG-AGGT 932
Db 756 GGTGAGTGTCTCTCCCAACAAAGTCTCTCACTCCACCACTGTGAGCAAAAGGGCAGT 697
QY 933 GGTGATAGAGTCA-GGGATCTATGCGCTTGGCCGCGAGCCG--ACCCCTTCCCTTTATC 989
Db 696 GGTGATAGAGTCAAGGGGTCTATGGCCCTTGTGCGAGCCGCGAGCCCTTCCCTTTAATC 637
QY 990 CTGCCACTGTCTATATGCTACCTTTCTATCTCTTCCCTCATCATCTTGTGTGGCATGA 1049
Db 636 CTGCCACTGTCTATATGCGACCTTTCTATCTCTTCCCTCATCATCTTGTGTGGCATCA 577
QY 1050 GGAGTGTGTATGTGAGAGAAATGGTTCGAGCTCAGAAAGATAAAAGATAAGTAGGTTAT 1109
Db 576 GCAGGTGGTCAATGTCAACCAATGGTTCGAGCTCAGAAAGATAAAAGATAAGTAGGTTAT 517
QY 1110 GCTGATCTCTTTTAAACCCCAAGATCAATCAAAATCCAGATGCTGGTCTCTATTCC 1169
Db 516 GCTGATCTCTTTTAAACCCCAAGATCAATCAATCNCAGATGCTGGTCTCTATTCC 457
QY 1170 CATGAAAAAGTCTCATGACATATTGAGAAGACCTACTTTACAAAGTGGCATATATTGCAA 1229
Db 456 CATGAAAAAGTCTCATGACATATTGAGAAGACCTACTTTACAAAGTGGCATATATTGCAA 397
QY 1230 TTTATTTTAAATAAGATACCTATTATATATTTCTTTATAGAAAAAAGTCTGGAGAG 1289
Db 396 TTTATTTTAAATAAGACACCTATTTCATATATTTCTTTATACAAAGATGAATTCCTGTATAAAAA 217
QY 1290 TTTACTTCAATGTAGCAATGTGAGGGTGAAGAGAGACATCATCTCTGATTTGCTCAGC 1469
Db 336 TTTACTTCAATGTAGCAATGTGAGGGTGGGAGATATAGGTGATTTTCTTTTAATTC 277
QY 1350 TGTAAATTTATCTGTATTTCTTAATTTTCTACAATGAAGATGAATTCCTGTATAAAAA 1409
Db 276 TGTAAATTTATCTGTATTTCTTAATTTTCTACAATGAAGATGAATTCCTGTATAAAAA 217
QY 1410 TAAGAAAAAATAATTTCTGAGGTGAAGAGAGAGACATCATCTCTGATTTGCTCAGC 1469
Db 216 TAAGAAAAAATAATTTCTGAGGTGAAGAGAGAGACATCATCTCTGATTTGCTCAGC 157
QY 1470 CTCGAATTCAGAGTAAATTCAAATGAAATCGAGCTCTGCTGCTCTGTTGGTTGTAG 1529
Db 156 CTCGAATTCAGAGTAAATTCAAATGAAATCGAGCTCTGCTGCTCTGTTGGTTGTAG 97
QY 1530 TAGTGATCAGGAAACAGATCTCAGCAACCCACTCAGGAGGAGGCTGTCTGAGTTGTG 1589
Db 96 TAGTGATCAGGAAACAGATCTCAGCAACCCACTCAGGAGGAGGCTGTCTGAGTTGTG 37
QY 1590 TGGCTGGAATCTCTGGGTAAAG 1611
Db 36 TGACTGCAATCTCTGGGTCAAG 15

RESULT 9
CA310393/c
LOCUS
DEFINITION
UI-H-Frl-big-n-18-0-UI-s1 NCI CGAP Frl Homo sapiens cDNA clone
UI-H-Frl-big-n-18-0-UI 3', mRNA sequence.
ACCESSION
CA310393
VERSION
CA310393.1 GI:24473447
KEYWORDS
EST.
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SOURCE	Homo sapiens (human)	Db	702	GTCTCTCAGGACCCCAAGCTGCTGACCTTAGTGGGCACTGACCACTTTGTCTTCTGGTTCCC	643
ORGANISM	Homo sapiens	Qy	647	AGTTTGCATAAATCTGAGATTTGGAGTCTAGTCAGGCTCTCCCCCACTGATGGTGC	706
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Db	642	AGTTTGGATAAATCTGAGA-TNGGAGTCTAGTCACGGTCTCCCCCACTGATGGTGC	584
AUTHORS	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	Qy	707	TACTGCTGGACCTTCTTAAACCAATCTGGGGTAAACTGGGAATAACATGAAGAATT	766
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	Db	583	TACTGCTGGGAATCTTGTAAACAACATGTGGGGTAAACTGGGAATAACATGAAGAATT	524
JOURNAL	Unpublished (1997)	Qy	767	TCGTGGGGGTGGGGTGGGGAGTCTGGGAATCAATCTCTGCTTAATGTAATGACCAAG	826
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a> Tissue Procurement: Dr. Gary W. Hunninghake, U of I cDNA library preparation: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, <a href="mailto:bento-soares@uiowa.edu">bento-soares@uiowa.edu</a> The following repetitive elements were found in this cDNA sequence: 1-61, >AT-rich#Low_complexity Seq primer: M13 FORWARD POLYA=Yes.	Db	523	TCGTGGAGGTGGGGTGGGGAGTGGTGGGAATCATCTCTGCTTAATGTAATGACCAAG	464
		Qy	827	TGTTACCTTGAGCCCGCAGGCAACCCATCCCACTTGGAGCTTATAGGGTCAGTAGCT	886
		Db	463	TGTTACCTTGAGCCCGCAGGCAACCCATCCCACTTGGAGCTTATAGGGTCAGTAGCT	404
		Qy	887	CTCCACATGAGTCTCTCACTCACTCACTGTCGACGAGGAGGAGTGGTCATAGAGTCAG	946
		Db	403	CTCCACATGAGACCTGTCACTCACTCACTGTCGACGAGGAGGAGTGGTCATAGAGTCAG	344
		Qy	947	GGATCTATGGCCCTTGGGCCAGCCCACTTCCCTTT-ATCCTGCCACTGTCTATATG	1005
		Db	343	GGATCTATGGCCCTTGGGCCAGCCCACTTCCCTTTATCTCTGCCACTGTCTATATG	284
		Qy	1006	CTACCTTTCTATCTCTCCCTCATCATCTTGTGTGGGCATGAGAGTGGTGTCTCA	1065
		Db	283	CTACCTTTCTATCTCTCCCTCATCATCTTGTGTGGGCATGAGAGTGGTGTCTCA	224
		Qy	1066	GAAGAATGTTGAGCTCAGAAGATAAAGATAGTAGGGTATGCTGATCTCTTTAA	1125
		Db	223	GAAGAATGTTGAGCTCAGAAGATAAAGATAGTAGGGTATGCTGATCTCTTTAA	164
		Qy	1126	AAACCCAGATACATCAAAATCCAGATGCTGCTCTTATTTCCCATGAAAAGTCTCA	1185
		Db	163	AAACCCAGATACATCAAAATCCAGATGCTGCTCTTATTTCCCATGAAAAGTCTCA	104
		Qy	1186	TGACATATTGGAAGACCTTACTTACAAAGTGCAATATTTGCAATTTATTTAATFAAA	1245
		Db	103	TGACATATTGGAAGACCTTACTTACAAAGTGCAATATTTGCAATTTATTTAATFAAA	44
		Qy	1246	GATACCTATTATATATTTCTTTATAGAAAAA	1278
		Db	43	GATACCTATTATATATTTCTTTATAGAAAAA	11
RESULT 10					
BF509095/c					
LOCUS	UI-H-B14-acu-e-01-0-UI-s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086280 3', mRNA sequence.				
DEFINITION	BF509095				
ACCESSION	BF509095.1				
VERSION	EST.				
KEYWORDS	BF509095.1				
SOURCE	EST.				
ORGANISM	Homo sapiens (human)				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 697)				
AUTHORS	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .				
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
JOURNAL	Unpublished (1997)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a> The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://www-bio.11nl.gov/bbrp/image/image.html">www-bio.11nl.gov/bbrp/image/image.html</a> The following repetitive				

ORIGIN

Query Match 25.2%; Score 644.6; DB 6; Length 702;  
Best Local Similarity 97.4%; Pred. No. 2.4e-155;  
Matches 675; Conservative 0; Mismatches 16; Indels 2; Gaps 2;  
QY 587 GTCTCAGGACCCCAAGCTGACTAGTGGGCACTGACCACTTTGTCTTCTGGTTCCC  
|||||



elements were found in this cDNA sequence: 1-60,

>AT rich#Low complexity

Seq primer: M13 Forward

POLVA=Yes.

## FEATURES

source

Location/Qualifiers

1..697

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3086280"

/lab\_host="DH10B (Life Technologies)"

/clone\_lib="NCI\_CGAP\_Sub8"

/notes="Vector: pT773D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; NCI CGAP Sub8

is a subcloned library derived from NCI CGAP Subs. The

NCI CGAP Sub8 library had 2.5 million recombinants. A

single-stranded DNA preparation of NCI\_CGAP\_Subs was used

as a tracer in a subtractive hybridization with a driver

comprising: a pool of clones from NCI CGAP Subs (IMAGE

clone Ids 2732833-2737415, 3068040-3069191; 25% of the

driver population), a pool of clones from NCI CGAP Sub4

(IMAGE clone Ids 2723592-2729326; 25% of the driver

population), NCI CGAP Sub6 (pool AIF-AJU, IMAGE Ids

2728969-2733190; 25% of the driver population), and

NCI CGAP Sub7 (IMAGE Ids 3069192-3072238,

3081864-3084550; 25% of the driver population).

Subtraction was performed as previously described

[Bonaldi, Lennon & Soares (1996): Normalization and

Subtraction: Two Approaches To Facilitate Gene Discovery.

Genome Research 6, 791-806.

TAG TISSUE=lung

TAG LIB=NCI CGAP\_Lu19

TAG\_SEQ=GACGAC

## ORIGIN

Query Match 25.1%; Score 643.2; DB 2; Length 697;

Best Local Similarity 97.7%; Pred. No. 5.6e-155;

Matches 673; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

QY 591 TCAGGACCCCGAGTCTGACTTAGTGGGACCTGACCACTTTGCTCTGTTCCCGATT 650

DB 697 TCAGGACCCCGAGTCTGACTTAGTGGGACCTGACCACTTTGCTCTGTTCCCGATT 638

QY 651 TGCATAAATCTGAGATTTGGAGCTCAGTCCAGGGTCTCTCCCACTGGATGGTGTCT 710

DB 637 TGCATAAATCTGAGATTT-GAGCTCAGTCCAGGGTCTCTCCCACTGGATGGTGTCT 579

QY 711 GCTGTGGAACCTGTAAAAACCATGTGGGGTAAACTGGGAATAACATGAAAAAGATTCTG 770

DB 578 GCTGTGGAATCTGTAAAAACCATGTGGGGTAAACTGGGAATAACATGAAAAAGATTCTG 519

QY 771 TGGGGTGGGGTGGGGAGTGTGGGAATCATCTCTGTTAATGGTAACTGCAAGTGT 830

DB 518 TGGAGTGGGGTGGGGAGTGTGGGAATCATCTCTGTTAATGGTAACTGCAAGTGT 459

QY 831 ACCCTGAGCCCGCAGGCCAACCCATCCCGAGTTGAGCCCTTATAGGCTCAGTAGCTCTCC 890

DB 458 ACCCTGAGCCCGCAGGCCAACCCATCCCGAGTTGAGCCCTTATAGGCTCAGTAGCTCTCC 399

QY 891 ACATGAAGTCTCTCATCTACCACTGTGAGGAGGGAGGTGGTTCATAGATCAGGGAT 950

DB 398 ACATGAAGACCTGTCTACTCACCCTATGAGGAGGGAGGTGGTTCATAGATCAGGGAT 339

QY 951 CTATGSCCTTGGCCAGCCCAACCCCTTCCCTTT-ATCCTGCCACTGTCTATATGCTAC 1009

DB 338 CTATGSCCTTGGCCAGCCCAACCCCTTCCCTTTAATCTGCCACTGTCTATATGCTAC 279

QY 1010 CTTTCCTATCTCTCCCTCATCTTGTGTGGCATCAGGAGGTGGTGTCTCAGAG 1069

DB 278 CTTTCCTATCTCTCCCTCATCTTGTGTGGCATCAGGAGGTGGTGTCTCAGAG 219

QY 1070 AAATGGTTCGAGCTCAGAGATAAAGATAAGTAGGGTATGCTGATCTCTTTTAAAAAC 1129

DB 218 AAATGGTTCGAGCTCAGAGATAAAGATAAAGATAAGTAGGGTATGCTGATCTCTTTTAAAAAC 159

QY 1130 CCAAGATACAATCAAAATCCAGATGCTGCTCTATTCCCATGAAAAGTCTCATGAC 1189

DB 158 CCAAGATACAATCAAAATCCAGATGCTGCTCTATTCCCATGAAAAGTCTCATGAC 99

QY 1190 ATATTGAGAAGACCTACTTACAAAGTGGCATATATTGCAATTTATTTTAAATAAGATA 1249

DB 98 ATATTGAGAAGACCTACTTACAAAGTGGCATATATTGCAATTTATTTTAAATAAGATA 39

QY 1250 CCTATTATATATTTCTTTATAGAAAAA 1278

DB 38 CCTATTATATATTTCTTTATAGAAAAA 10

## RESULT 11

BI090567

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

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COMMENT

COMMENT

Qy	181	ATGCCAGCGTGTCCCGCGTCTATCTCGGTGTCCAGGTGGGAAGCCAGTGCCTGTCAATGTG	240
Db	286	ATGCCAGCGTGTCCCGCGTCTATCTCGGTGTCCAGGTGGGAAGCCAGTGCCTGTCAATGTG	345
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Db	346	GGGTGGGGCAGGAGCCGACCTCTAACACTTAGAGCCAGTGAACATCATGGAGCTCTATCTTG	405
Qy	301	GTGCCAAGGAATCCAAAGAGCTTACCTTTCTACCCGGCGGACATGGGGCTCACCTCCAGCT	360
Db	406	GTGCCAAGGAATCCAAAGAGCTTACCTTTCTACCCGGCGGACATGGGGCTCACCTCCAGCT	465
Qy	361	TCGAGTGGCGCTCTACCCGGCGTGGTTCCTGTGTGCA CGTGCCTGAAGCCGATCAGCCTG	420
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Qy	421	TCAGACTCACCCAGCTTCCCGAGAAATGGTGGCTGGAAATGCCCCATCACAGACTTCTACT	480
Db	526	TCAGACTCACCCAGCTTCCCGAGAAATGGTGGCTGGAAATGCCCCATCACAGACTTCTACT	585
Qy	481	TCCAGCAGTGTGAATAGGGCAACGTGCCCGCCAGAACTCCCTGGGAGAGCCAGCTCGG	540
Db	586	TCCAGCAGTGTGAATAGGGCAAC-AGTGCCCGCCAGAACTCCCTGGGAGAGCCAGCTCGG	644
Qy	541	GTGAGGGGTGAGTGGAGAGACCCATAGCGCGAGCAATCACTTTCTTGTCTTCAGAGACCC	600
Db	645	GTGAGGGGTGAGTGGAGAGACCCATAGCGCGAGCAATCACTTTCTTGTCTTCAGAGACCC	704
Qy	601	CAGCTGTGACTTACTGGGCACTGACCACTTTGTCTTCTGGTCCAGTTCATTAATTT	660
Db	705	CA-GTCTGACTTAAGAGAGGAACCTTGACAACCTTGGCTTCTGGTCCAGTTTGGATAATTT	763
Qy	661	CTGAGATTTGGAGTCTAGTCCAGGGTCTCTCCCGCACTGGATGGTGTCTACTCTGTGGAAC	720
Db	764	GACATAGGAGCTCCAGGTCCACGGTACTCAGAAATGGATGGAGCTACTGGTGTGNAAC	823
Qy	721	CTTGTAATAAACCAATGGGGTAAACTGGGA	750
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LOCUS			
DEFINITION			
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Clone CSOD1013YA07 3-PRIME, mRNA sequence.			
ACCESSION			
BX350083			
VERSION			
BX350083.2 GI:46533561			
KEYWORDS			
EST.			
SOURCE			
Homo sapiens (human)			
ORGANISM			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE			
1. (bases 1 to 915)			
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.			
Full-length cDNA libraries and normalization			
Unpublished (2001)			
COMMENT			
On May 5, 2003 this sequence version replaced gi:30383465.			
Contact: Genoscope			
Genoscope - Centre National de Sequencage			
2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE			
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr			
1st strand cDNA was primed with a NotI-oligo(qt) primer. Five primer			
end enriched, double-strand cDNA was digested with NotI and cloned			
into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library			
was normalized. Library was constructed by Life Technologies, a			
division of Invitrogen. This sequence belongs to sequence cluster			
1383.f			
For more information about this cluster, see			
http://www.genoscope.cns.fr/cdna?b=CS0BA1018ZD02_CS01644_2&c=1383.f			
FEATURES			
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Best Local Similarity	87.0%; Pred. No. 3.6e-131;
Matches 617; Conservative 0; Mismatches 91; Indels 1; Gaps 1;	
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Qy	975 CCCCTTCCCTTTATCTCTGCCACTGTCTATGCTACCTTTCCTATCTCTTCCCTCATCATC 1034
Db	649 TTAATCCCTGCCACTGTCAAAATGTAACCTTTCCTATCTCTTCCCTCAATCATCTT 590
Qy	1035 TTGTTGGGCATGAGAGGTGGTGATGTGAG-AAGAAATGGTTCGAGCTCAGAAGATAA 1093
Db	589 GGTGTGGGCATGAGGAGGGTGTGATGTGAGAAAGAAATGGTCGAGCTCAGAAGATAA 530
Qy	1094 AAGTAAGTAGGGTATGCTGATCCTCTTTTAAAAACCCAGATACATCAAAATCCCAGA 1153
Db	529 AAGTAAGTAGGGTATGCTGATCCTCTTTTAAAAACCCAGATACATCAAAATCCCAGA 470
Qy	1154 TGCTGGTCTCTATTCCCATGAAAAGTGCTCATGACATATTGAGAAGACCTACTTACAAA 1213
Db	469 TGCTGGTCTCTATTCCCATGAAAAGTGCTCATGACATATTGAGAAGACCTACTTACAAA 410
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Qy	1334 ATTTTCTTTTAAATCTGTAAATTTATCTGATTTTCTTAATTTTCTACAATGAAGATGA 1393
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Qy	1514 CTCTGGTTGGTGTGTAGTAGTATCAGAAAACAGATCTCAGCAAGCCACTGAGGAGGAGG 1573
Db	109 CTCTGGTTGGTGTGTAGTAGTATCAGAAAACAGATCTCAGCAAGCCACTGAGGAGGAGG 50
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DEFINITION	sequence.
ACCESSION	AUI138695
VERSION	AUI138695.1 GI:11000216
KEYWORDS	EST.

**FEATURES**  
**SOURCE**

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SOURCE      Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1 (bases 1 to 555)
AUTHORS      Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
              Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
              Isogai,T.
TITLE        HRI human cDNA project
JOURNAL      Unpublished (2000)
COMMENT      Contact: Takao Isogai
              Genomics Laboratory
              1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
              Tel: 81-438-52-3975
              Fax: 81-438-52-3986
              Email: genomics@hri.co.jp
              HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
              Research Institute; cDNA library construction: Department of
              Virology, Institute of Medical Science, University of Tokyo, and
              Helix Research Institute.
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  QY 755 CATGAAGAATTTCTGGGGTGGGGTGGGGAGTCTGGGAATCATCTTCCTTAATG 814
  DB 61 CATGAAGAATTTCTGGGGTGGGGTGGGGAGTGGTGGGAATCATCTTCCTTAATG 120
  QY 815 GTAACATGACAAGTGTACCTGAGCCCGCAGCCCAACCCATCCCGAGTTGAGCCTTATA 874
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  DB 181 GGGTCAGTAGCTTCCACATGAAGTCTCTCACTACCACTGTCAGGAGAGGGAGGTGG 240
  QY 935 TCATAGAGTCAGGATCTATGGCCCTTGGCCAGCCGCCACCCCTTCCCTTT-ATCCTGC 993
  DB 241 TCATAGAGTCAGGATCTATGGCCCTTGGCCAGCCGCCACCCCTTCCCTTTAATCCTGC 300
  QY 994 CACTGTCATATGCTACTCTTCCCTATCTCTTCCCTCATCATCTTGTGTGGGATGAGGAG 1053
  DB 301 CACTGTCATATGCTACTCTTCCCTATCTCTTCCCTCATCATCTTGTGTGGGATGAGGAG 360
  QY 1054 GTGGTGTATGTAGAAGAAATGGTTGAGCTCAGAGATAAAGATAAGTAGGGTATGCTG 1113
  DB 361 GTGGTGTATGTAGAAGAAATGGTTCAGCTCAGAGATAAAGATAAATAGGTATGCTG 420
  QY 1114 ATCCCTCTTTAAACCCAGATACATCAATCCAGATCGTGTCTTATTCCTCCATG 1173
  DB 421 ATCCCTCTTTAAACCCAGATACATCAATCCAGATCGTGTCTTATTCCTCCATG 480
  QY 1174 AAAAAGTGTCTATGACATATGAGAAGACCTACTTACAAAGTGGCATATATTGCAATTTA 1233
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541 TTTTAATTAAGAAT 555

RESULT 14
BQ351235
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
PUBMED
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=RC0&t2=RC0-HT0773-
010600-021-e07&t3=2000-06-01&t4=1)
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High quality sequence start: 14
High quality sequence stop: 555.
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/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0773"
/note="Organ: head neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
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  DB 27 AGATATAGTACGTTAAGACNAGTCTATGCTGATGAGTAGACCGTAAATTCATATGA 86
  QY 1851 CTGGTTTCCTTGTATGAAAAAGAGAGGACACACAGACAGAGGAGCGGGGAAGACTAT 1910
  DB 87 CTGGTTTCCTTGTATCAAAAAGGAGAGGACACACAGACAGAGGATGCGGGGAAGACTAT 146
  QY 1911 GTAAAGATCAAGCGAGATCGAGTCTTTCAGCCACCAAGCTTAAGAAACACCAAGGATG 1970
  DB 147 GTAAAGATCAAGCGAGATCGAGTCTTTCAGCCACCAAGCTTAAGAAACACCAAGGATG 206
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 13, 2005, 10:45:20 ; Search time 21.27 Seconds  
(without alignments)  
10854.228 Million cell updates/sec

Title: US-09-617-720A-2

Perfect score: 39

Sequence: 1 ttgaggacagcagactccacagctccgccagagaa 39

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: Geneseqn1990s.\*  
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5: Geneseqn2001bs.\*  
6: Geneseqn2002as.\*  
7: Geneseqn2002bs.\*  
8: Geneseqn2003as.\*  
9: Geneseqn2003bs.\*  
10: Geneseqn2003cs.\*  
11: Geneseqn2003ds.\*  
12: Geneseqn2004as.\*  
13: Geneseqn2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	100.0	39	AAF27922	Human IL-
2	37.4	95.9	54	AAF27927	Interleukin
3	37.4	95.9	2720	ADN05043	Adn05043 Antipsori
4	37.4	95.9	5751	AAF31355	Abz77450 Genomic C
5	37.4	95.9	5751	ABZ77450	Genomic D
6	37.4	95.9	5752	AAZ30052	DNA encod
7	37.4	95.9	6540	AAF27950	Interleuk
8	37.4	95.9	7605	AAZ30053	DNA encod
9	37.4	95.9	7605	AAF31356	Extension
10	37.4	95.9	7605	ABZ77451	Extended
11	22.8	58.5	3071	ABL26414	Drosophil
12	22.6	57.9	49087	ACN44492	Mouse gen
13	22.4	57.4	689	AAK61778	Human imm
14	22.4	57.4	7667	AAZ27743	DNA encod
15	22.4	57.4	7667	AAK82163	Human imm
16	22.4	57.4	7667	AAK80991	Human imm
17	22.4	57.4	7667	10 ADB94546	Novel hum
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19	22.4	57.4	38764	10 ADB72758	Human RAC
20	22.4	57.4	38764	10 ADC85500	Human RAC

C 21	22.4	57.4	38764	12	ADM74615	Adm74615 Human ear
C 22	22.2	56.9	378	9	ACH47270	ACH47270 Human inf
C 23	22	56.4	98546	11	ACN44790	ACN44790 Human gen
C 24	21.6	55.4	1311	5	AAS67806	AAS67806 DNA encod
C 25	21.6	55.4	1830	5	AAS67805	AAS67805 DNA encod
C 26	21.6	55.4	2100	5	AAH25997	Human PAL
C 27	21.6	55.4	2100	10	ADF69161	Human MP5
C 28	21.6	55.4	5397	4	ABL20241	ABL20241 Drosophil
C 29	21.6	55.4	28491	4	ABL20240	ABL20240 Drosophil
C 30	21.4	54.9	1092	5	AAS81578	AAS81578 DNA encod
C 31	21.4	54.9	276820	11	ADP75188	ADP75188 Human ADA
C 32	21.2	54.4	2064	10	ADB62042	ADB62042 Human cDN
C 33	21.2	54.4	5159	8	ACC46691	ACC46691 Human dit
C 34	21.2	54.4	6020	12	ADJ12607	ADJ12607 DNA fragm
C 35	21.2	54.4	110000	13	ABD32780_3	Continuation (4 of
C 36	21.2	54.4	11441	12	ADQ21090	ADQ21090 Human sof
C 37	21	53.8	391	3	AAC02974	AAC02974 Human sec
C 38	21	53.8	913	6	ABL48933	ABL48933 Ovarian c
C 39	21	53.8	1549	6	ABK49709	ABK49709 cDNA enco
C 40	21	53.8	2487	9	ACD26637	ACD26637 Human sec
C 41	21	53.8	2490	3	AAZ50813	AAZ50813 Human TAN
C 42	21	53.8	11646	4	ADQ98220	ADQ98220 Human ext
C 43	21	53.8	11646	4	AAK70925	AAK70925 Human imm
C 44	21	53.8	14148	4	AAK70926	AAK70926 Human imm
C 45	20.8	53.3	1272	4	AAH99081	AAH99081 Human EST

## ALIGNMENTS

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AC AAF27922;  
XX  
DT 08-MAY-2001 (first entry)  
XX  
DE Human IL-1L1 coding sequence 5' end #1.  
XX  
KW Human; IL-1L1; interleukin-1 locus; IL-1beta; IL-1receptor; psoriasis;  
KW chromosome 2q13; inflammatory disease; heart disease; Graves' disease;  
KW rheumatoid arthritis; inflammatory bowel disorder; diabetes; cancer;  
KW osteoporosis; systemic lupus erythematosus; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200105974-A2.  
XX  
PD 25-JAN-2001.  
XX  
PF 17-JUL-2000; 2000WO-US019508.  
XX  
PR 16-JUL-1999; 99US-0144298P.  
PA (INTE-) INTERLEUKIN GENETICS INC.  
PI Nicklin M, Barton J;  
XX  
DR WPI; 2001-091974/10.  
XX  
PT Nucleic acids encoding human and murine interleukin-1L1 polypeptides  
PT useful for controlling inflammatory processes.  
XX  
PS Claim 20; Fig 1; 150pp; English.  
XX  
CC The present invention provides the protein and coding sequences of the  
CC human and murine interleukin-1L1 (IL-1L1) proteins. The IL-1L1 gene is  
CC located between the IL-1beta and IL-1receptor genes at human chromosome  
CC 2q13. The sequences are useful in the diagnosis, prevention and treatment  
CC of heart disease, cancer and inflammatory diseases such as rheumatoid  
CC arthritis, systemic lupus erythematosus, inflammatory bowel disorder,  
CC diabetes, psoriasis, osteoporosis, lichen sclerosis, ulcerative colitis,

CC severe periodontal disease and pregnancy complications. The present  
CC sequence is one of two alternative 5' ends of the human IL-1L1 coding  
CC sequence  
XX  
SQ Sequence 39 BP; 12 A; 12 C; 11 G; 4 T; 0 U; 0 Other;  
Query Match 100.0%; Score 39; DB 5; Length 39;  
Best Local Similarity 100.0%; Pred. No. 6.7e-05;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 TTGAGGAACAGGAGAGCTCCACAGCTCCCGCCAGGAGAA 39  
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AAF27927  
ID AAF27927 standard; DNA; 54 BP.  
XX  
AC AAF27927;  
XX  
DT 08-MAY-2001 (first entry)  
XX  
DE Interleukin-1L1 coding sequence fragment #2.  
XX  
KW Human; IL-1L1; interleukin-1 locus; IL-1beta; IL-1receptor; psoriasis;  
KW chromosome 2q13; inflammatory disease; heart disease; Graves' disease;  
KW rheumatoid arthritis; inflammatory bowel disorder; diabetes; cancer;  
KW osteoporosis; systemic lupus erythematosus; ds.  
XX  
OS Unidentified.  
XX  
PN WO200105974-A2.  
XX  
PD 25-JAN-2001..  
XX  
PF 17-JUL-2000; 2000WO-US019508.  
XX  
PR 16-JUL-1999; 99US-0144298P.  
XX  
PA (INTE-) INTERLEUKIN GENETICS INC.  
XX  
PI Nicklin M, Barton J;  
XX  
DR WPI; 2001-091974/10.  
XX  
PT Nucleic acids encoding human and murine interleukin-1L1 polypeptides  
PT useful for controlling inflammatory processes.  
XX  
PS Example; Fig 10; 150pp; English.  
XX  
CC The present invention provides the protein and coding sequences of the  
CC human and murine interleukin-1L1 (IL-1L1) proteins. The IL-1L1 gene is  
CC located between the IL-1beta and IL-1receptor genes at human chromosome  
CC 2q13. The sequences are useful in the diagnosis, prevention and treatment  
CC of heart disease, cancer and inflammatory diseases such as rheumatoid  
CC arthritis, systemic lupus erythematosus, inflammatory bowel disorder,  
CC diabetes, psoriasis, osteoporosis, lichen sclerosis, ulcerative colitis,  
CC severe periodontal disease and pregnancy complications. The present  
CC sequence is an IL-1L1 coding sequence fragment  
XX  
SQ Sequence 54 BP; 17 A; 14 C; 16 G; 7 T; 0 U; 0 Other;  
Query Match 95.9%; Score 37.4; DB 5; Length 54;  
Best Local Similarity 97.4%; Pred. No. 0.00027;  
Matches 38; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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DB 2 TGGAGGAACAGGAGAGCTCCACAGCTCCCGCCAGGAGAA 40  
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AC ADN05043;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
DE Antipsoriatic cDNA sequence #737.  
XX  
KW ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.  
XX  
OS Homo sapiens.  
XX  
PN WO2004028479-A2.  
XX  
PD 08-APR-2004.  
XX  
PF 25-SEP-2003; 2003WO-US030907.  
XX  
PR 25-SEP-2002; 2002US-0414006P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;  
PI Wu ID;  
XX  
DR WPI; 2004-305105/28.  
DR P-PSDB; ADN05044.  
XX  
PT New PRO nucleic acid or polypeptide, useful for preparing a  
PT pharmaceutical composition for diagnosing or treating psoriasis in a  
PT mammal.  
XX  
PS Claim 1; SEQ ID NO 1437; 3069pp; English.  
XX  
CC The invention relates to novel polynucleotide and polypeptides for  
CC treating psoriasis or a sequence having at least 80% identity to the  
CC above sequences. The nucleic acid is useful for preparing a composition  
CC for diagnosing or treating psoriasis in a mammal. This sequence  
CC corresponds to one of the polynucleotides of the invention.  
XX  
SQ Sequence 2720 BP; 735 A; 621 C; 671 G; 693 T; 0 U; 0 Other;  
Query Match 95.9%; Score 37.4; DB 12; Length 2720;  
Best Local Similarity 97.4%; Pred. No. 0.0004;  
Matches 38; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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DB 83 TGGAGGAACAGGAGAGCTCCACAGCTCCCGCCAGGAGAA 121  
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XX  
AC AAF31355;  
XX  
DT 05-APR-2001 (first entry)  
XX  
DE Genomic clone B2HFLS20W.  
XX  
KW Interleukin; IL-1 receptor; cancer; inflammation; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200102571-A2.  
XX  
PD 11-JAN-2001.  
XX  
PF 07-JUL-2000; 2000WO-US018710.  
XX  
PR 07-JUL-1999; 99US-00348942.



PR 13-OCT-1999; 99US-00417455.  
PR 08-DEC-1999; 99US-00457626.  
PR 10-MAR-2000; 2000US-00523552.  
PR 22-MAY-2000; 2000US-00576008.  
XX (HYSE-) HYSEQ INC.  
XX Ford J, Pace A;  
PI WPI; 2001-071582/08.  
XX  
XX Isolated nucleic acids encoding interleukin-1 (IL-1) receptor antagonist  
PT proteins (referred as IL-1hYl), useful in the treatment of cancer, e.g.  
PT breast adenocarcinoma and brain tumors, and an inflammatory disease  
PT mediated by IL-18.  
XX  
XX Claim 1; Fig 9; 179pp; English.  
XX  
XX The present invention relates to interleukin (IL)-1 receptor antagonist  
CC proteins. IL-1hYl is useful for treating cancer, an inflammatory disease  
CC mediated by IL-18, inflammation resulting from infection or allergic  
CC reactions, and inflammation associated with chronic bronchitis,  
CC arthritis, diabetes or endothermia  
XX  
SQ Sequence 5751 BP; 1466 A; 1274 C; 1489 G; 1383 T; 0 U; 139 Other;  
Query Match 95.9%; Score 37.4; DB 4; Length 5751;  
Best Local Similarity 97.4%; Pred. No. 0.00043;  
Matches 38; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 TTGAGGACAGGAGACTCCACAGCTCCCGCCAGGAGAA 39  
DB 813 TGGAGGACAGGAGACTCCACAGCTCCCGCCAGGAGAA 851  
RESULT 5  
AB277450  
ID AB277450 standard; cDNA; 5751 BP.  
XX  
XX AB277450;  
AC  
XX 28-MAY-2003 (first entry)  
DT  
XX Genomic DNA sequence of a human Interleukin-1hYl (IL-1hYl).  
DE  
XX Interleukin-1hYl; IL-1hYl; B-cell proliferation; B-cell activation;  
XX B-cell differentiation; B-cell-related disorder; lymphoma; leukemia;  
KW myeloma; infection; autoimmune disease; allergy; asthma;  
KW allergic rhinitis; IGA production; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2003010291-A2.  
PN  
XX  
XX 06-FEB-2003.  
PD  
XX  
XX 25-JUL-2002; 2002WO-US023845.  
PF  
XX  
XX 25-JUL-2001; 2001US-0307754P.  
PR  
XX 29-NOV-2001; 2001US-0334668P.  
PR  
XX (HYSE-) HYSEQ INC.  
PA  
XX Ho AS, Lin H, Ford JE, Rupp F;  
PI  
XX WPI; 2003-239438/23.  
XX  
XX Inhibiting or stimulating B-cell proliferation, activation or  
PT differentiation, useful for treating B-cell-related disorders or  
PT autoimmune diseases, comprises administering an interleukin-1hYl  
PT polypeptide or its inhibitor.  
XX  
XX Disclosure; Page 109-111; 115pp; English.

XX The present sequence encodes human interleukin (IL)-1hYl polypeptide. IL-  
CC 1hYl inhibitors are used in the method of the invention. The  
CC specification describes a method of inhibiting B-cell proliferation,  
CC activation or differentiation. The method comprises administering an  
CC inhibitor of IL-1hYl activity to a human with elevated B-cell levels or  
CC activity, in an amount that inhibits B-cell proliferation induced by IL-  
CC 1hYl. The method is useful for inhibiting or stimulating B-cell  
CC proliferation, activation or differentiation in patients having a B-cell-  
CC related disorder (e.g. lymphoma, leukemia, myeloma or infection) or an  
CC autoimmune disease (e.g. allergy, asthma or allergic rhinitis), or in  
CC screening for compounds that modulate B-cell differentiation. The IL-1hYl  
CC polypeptide, or the inhibitor of IL-1hYl activity, is useful in preparing  
CC a medicament for stimulating or reducing B-cell proliferation.  
CC differentiation or activation. The IL-1hYl polypeptide may also be used  
CC in preparing a medicament for reducing IGA production  
XX  
SQ Sequence 5751 BP; 1466 A; 1274 C; 1489 G; 1383 T; 0 U; 139 Other;  
Query Match 95.9%; Score 37.4; DB 8; Length 5751;  
Best Local Similarity 97.4%; Pred. No. 0.00043;  
Matches 38; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 TTGAGGACAGGAGACTCCACAGCTCCCGCCAGGAGAA 39  
DB 813 TGGAGGACAGGAGACTCCACAGCTCCCGCCAGGAGAA 851  
RESULT 6  
AAZ30052  
ID AAZ30052 standard; DNA; 5752 BP.  
XX  
XX AAZ30052;  
AC  
XX 26-JAN-2000 (first entry)  
DT  
XX DNA encoding a human interleukin-1 receptor antagonist.  
DE  
XX Human; interleukin-1 receptor; IL-1; antagonist; sepsis;  
KW acute pancreatitis; endotoxin shock; cytokine induced shock;  
KW rheumatoid arthritis; chronic inflammatory arthritis;  
KW pancreatic cell damage; diabetes mellitus type 1;  
KW graft versus host disease; inflammatory bowel disease; inflammation;  
KW pulmonary disease; autoimmune disease; inflammatory disease;  
KW antiproliferative; myelogenous leukemia; premature labor;  
KW intrauterine infection; nutritional activity;  
KW hematopoiesis regulating activity; tissue growth activity;  
KW activin activity; inhibin activity; chemotactic activity;  
KW chemokinetic activity; hemostatic activity; thrombolytic activity;  
KW anti-inflammatory activity; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO9951744-A2.  
PN  
XX  
XX 14-OCT-1999.  
PD  
XX  
XX 05-APR-1999; 99WO-US004291.  
PF  
XX  
XX 03-APR-1998; 98US-00055010.  
PR  
XX 15-MAY-1998; 98US-00079909.  
PR  
XX 20-MAY-1998; 98US-00082364.  
PR  
XX 19-JUN-1998; 98US-00099818.  
PR  
XX 31-JUL-1998; 98US-00127698.  
PR  
XX 13-JAN-1999; 99US-00229591.  
PR  
XX 17-FEB-1999; 99US-00251370.  
PR  
XX (HYSE-) HYSEQ INC.  
PA  
XX Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;  
PI Leshkowitz D, Kita D, Ford J, Pace A, Alfenito M;  
PI  
XX WPI; 1999-611042/52.  
DR

XX New isolated interleukin-1 receptor binding polypeptides, used to treat  
 PT e.g. sepsis, shock, arthritis, pancreatitis, graft-versus-host disease,  
 PT inflammatory disease, autoimmune disease or proliferative disease.  
 XX  
 PS Claim 1; Fig 9A-C; 123pp; English.  
 XX  
 CC The present sequence encodes a human interleukin-1 (IL-1) receptor  
 CC antagonist. It represents the genomic sequence of AAZ30048-51. The  
 CC encoded polypeptide is capable of binding IL-1 receptors (IL-1Rs). The  
 CC polynucleotides and polypeptides can be used for the prevention or  
 CC treatment of disorders involving sepsis, acute pancreatitis, endotoxin  
 CC shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory  
 CC arthritis, pancreatic cell damage from diabetes mellitus type 1, graft  
 CC versus host disease, inflammatory bowel disease, inflammation associated  
 CC with pulmonary disease, other autoimmune disease or inflammatory disease,  
 CC an antiproliferative agent such as for acute or chronic myelogenous  
 CC leukemia or in the prevention of premature labor secondary to  
 CC intrauterine infections. They can also exhibit activities such as e.g.  
 CC nutritional activity, cytokine and cell proliferation/differentiation  
 CC activity, immune stimulating or suppressing activity, hematopoiesis  
 CC regulating activity, tissue growth activity, activin/inhibin activity,  
 CC chemotactic/chemokinetic activity, hemostatic and thrombolytic activity,  
 CC receptor/ligand activity, and anti-inflammatory activity. The products  
 CC can also be used for detection, diagnosis and drug screening  
 XX  
 XX Sequence 5752 BP; 1467 A; 1274 C; 1489 G; 1383 T; 0 U; 139 Other;

Query Match 95.9%; Score 37.4; DB 2; Length 5752;  
 Best Local Similarity 97.4%; Pred. No. 0.00043;  
 Matches 38; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAGGAACAGGACGACTCCACAGCTCCCGCCAGGAGAA 39  
 DB 813 TGGAGGAACAGGACGACTCCACAGCTCCCGCCAGGAGAA 851

## RESULT 7

AAZ27950  
 ID AAF27950 standard; DNA; 6540 BP.

XX AAF27950;

XX 08-MAY-2001 (first entry)

XX Interleukin-1L1 genomic sequence.

XX Human; IL-1L1; interleukin-1 locus; IL-1beta; IL-1receptor; psoriasis;  
 KW chromosome 2q13; inflammatory disease; heart disease; Graves' disease;  
 KW rheumatoid arthritis; inflammatory bowel disorder; diabetes; cancer;  
 KW osteoporosis; systemic lupus erythematosus; ds.

XX Unidentified.

XX WO200105974-A2.

XX 25-JAN-2001.

XX 17-JUL-2000; 2000WO-US019508.

XX 16-JUL-1999; 99US-0144298P.

XX (INTE-) INTERLEUKIN GENETICS INC.

XX Nicklin M, Barton J;

XX WPI; 2001-091974/10.

XX Nucleic acids encoding human and murine interleukin-1L1 polypeptides  
 PT useful for controlling inflammatory processes.

XX Example; Fig 11; 150pp; English.

XX

CC The present invention provides the protein and coding sequences of the  
 CC human and murine interleukin-1L1 (IL-1L1) proteins. The IL-1L1 gene is  
 CC located between the IL-1beta and IL-1receptor genes at human chromosome  
 CC 2q13. The sequences are useful in the diagnosis, prevention and treatment  
 CC of heart disease, cancer and inflammatory diseases such as rheumatoid  
 CC arthritis, systemic lupus erythematosus, inflammatory bowel disorder,  
 CC diabetes, psoriasis, osteoporosis, lichen sclerosis, ulcerative colitis,  
 CC severe periodontal disease and pregnancy complications. The present  
 CC sequence is the IL-1L1 gene

XX Sequence 6540 BP; 1747 A; 1458 C; 1709 G; 1626 T; 0 U; 0 Other;

Query Match 95.9%; Score 37.4; DB 5; Length 6540;  
 Best Local Similarity 97.4%; Pred. No. 0.00044;  
 Matches 38; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAGGAACAGGACGACTCCACAGCTCCCGCCAGGAGAA 39  
 DB 970 TGGAGGAACAGGACGACTCCACAGCTCCCGCCAGGAGAA 1008

## RESULT 8

AAZ30053

ID AAZ30053 standard; DNA; 7605 BP.

XX AAZ30053;

XX 26-JAN-2000 (first entry)

XX DNA encoding a human interleukin-1 receptor antagonist.

XX Human; interleukin-1 receptor; IL-1; antagonist; sepsis;  
 KW acute pancreatitis; endotoxin shock; cytokine induced shock;  
 KW rheumatoid arthritis; chronic inflammatory arthritis;  
 KW pancreatic cell damage; diabetes mellitus type 1;  
 KW graft versus host disease; inflammatory bowel disease; inflammation;  
 KW pulmonary disease; autoimmune disease; inflammatory disease;  
 KW antiproliferative; myelogenous leukemia; premature labor;  
 KW intrauterine infection; nutritional activity;  
 KW hematopoiesis regulating activity; tissue growth activity;  
 KW activin activity; inhibin activity; chemotactic activity;  
 KW chemokinetic activity; hemostatic activity; thrombolytic activity;  
 KW anti-inflammatory activity; ss.

XX Homo sapiens.

XX WO9951744-A2.

XX 14-OCT-1999.

XX 05-APR-1999; 99WO-US004291.

XX 03-APR-1998; 98US-00055010.

XX 15-MAY-1998; 98US-00079909.

XX 20-MAY-1998; 98US-00082364.

XX 19-JUN-1998; 98US-00099818.

XX 31-JUL-1998; 98US-00127698.

XX 13-JAN-1999; 99US-00229591.

XX 17-FEB-1999; 99US-00251370.

XX (HYSE-) HYSEQ INC.

XX Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;

XX Leshkowitz D, Kita D, Ford J, Pace A, Alfenito M;

XX WPI; 1999-611042/52.

XX New isolated interleukin-1 receptor binding polypeptides, used to treat  
 PT e.g. sepsis, shock, arthritis, pancreatitis, graft-versus-host disease,  
 PT inflammatory disease, autoimmune disease or proliferative disease.  
 XX Disclosure; Fig 10A-C; 123pp; English.



QY 1 TTGAGGAACAGGAGACTCCACAGCTCCCGCCAGGAGAA 39  
 Db 1838 TGGAGGAACAGGAGACTCCACAGCTCCCGCCAGGAGAA 1876

RESULT 11  
 ABL26414  
 ID ABL26414 standard; DNA; 3071 BP.  
 XX  
 AC ABL26414;  
 DT 26-MAR-2002 (first entry)  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 30715.  
 KW Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical; gene; ds.  
 XX Drosophila melanogaster.  
 OS WO200171042-A2.  
 PN 27-SEP-2001.  
 PD 23-MAR-2001; 2001WO-US009231.  
 XX 23-MAR-2000; 2000US-0191637P.  
 PR 11-JUL-2000; 2000US-00614150.  
 XX (PEXE ) PE CORP NY.  
 PA Venter JC, Adams M, Li PWD, Myers EW;  
 PI WPI; 2001-656860/75.  
 DR New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signaling and cell-cell  
 PT interactions.  
 XX Claim 1; SEQ ID NO 30715; 21pp + Sequence Listing; English.

QY 4 AGGAACAGGAGACTCCACAGCTCCCGCCAGGAG 37  
 Db 337 AGGAACAGGAGACTCCATGGTCCCACTGGAG 370

RESULT 12  
 ACN44492/c  
 ID ACN44492 standard; DNA; 49087 BP.  
 XX  
 AC ACN44492;  
 DT 18-NOV-2004 (first entry)  
 DE Mouse genomic sequence MCG20206.

Query Match 58.5%; Score 22.8; DB 4; Length 3071;  
 Best Local Similarity 79.4%; Pred. No. 1.1e+02;  
 Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

XX Cytostatic; carcinoma; lymphoma; cancer; murine; gene; ss.  
 KW Mus musculus.  
 OS WO2003073826-A2.  
 PN 12-SEP-2003.  
 PD 28-FEB-2003; 2003WO-US006235.  
 PF 01-MAR-2002; 2002US-00087192.  
 XX (SAGR-) SAGRES DISCOVERY.  
 PA Morris DW;  
 PI WPI; 2003-328604/31.  
 DR Recombinant nucleic acid useful for diagnosis and treatment of carcinoma  
 PT comprises a nucleotide sequence.  
 XX Claim 1; SEQ ID NO 967; Opp; English.

CC The present invention relates to novel DNA and protein sequences which  
 CC are associated with carcinomas. The sequences are useful for: (i) for  
 CC screening drug candidates; (ii) for screening of bioactive agent capable  
 CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of  
 CC a bioactive agent capable of modulating the activity of CAP; (iv) for  
 CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing  
 CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating  
 CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;  
 CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for  
 CC determining Carcinoma Associated (CA) gene copy number. In addition, the  
 CC CA genes are useful as DNA vaccines and the CAP are useful as markers of  
 CC carcinoma including lymphoma. The present sequence is one such CA coding  
 CC sequence. Note: This patent is an equivalent to basic patent  
 CC US2002182586A1, for which no sequence data was published

QY 1 TTGAGGAACAGGAGACTCCACAGCTCCCGCCAGGAG 37  
 Db 41121 TTGAGGAACAGGAGACTCCCTCTTAGGAG 41085

RESULT 13  
 AAK61778/c  
 ID AAK61778 standard; cDNA; 689 BP.  
 XX  
 AC AAK61778;  
 DT 06-NOV-2001 (first entry)  
 XX Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:6838.  
 DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
 KW cytostatic; gene therapy; vaccine; metastasis; ss.  
 XX Homo sapiens.  
 OS WO200157182-A2.  
 PN 09-AUG-2001.  
 PD 17-JAN-2001; 2001WO-US001354.  
 PF 31-JAN-2000; 2000US-0179065P.  
 PR 04-FEB-2000; 2000US-0180628P.

Query Match 57.9%; Score 22.6; DB 11; Length 49087;  
 Best Local Similarity 75.7%; Pred. No. 1.7e+02;  
 Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

PR 24-FEB-2000; 2000US-0184564P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 11-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 14-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225366P.  
PR 14-AUG-2000; 2000US-0225367P.  
PR 14-AUG-2000; 2000US-0225368P.  
PR 14-AUG-2000; 2000US-0225370P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226688P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 08-SEP-2000; 2000US-0231414P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
PR 14-SEP-2000; 2000US-0233064P.  
PR 14-SEP-2000; 2000US-0233065P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
PR 25-SEP-2000; 2000US-0234998P.  
PR 26-SEP-2000; 2000US-0235484P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235836P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.

PR 02-OCT-2000; 2000US-0237039P.  
PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239935P.  
PR 13-OCT-2000; 2000US-0239937P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241221P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241786P.  
PR 20-OCT-2000; 2000US-0241787P.  
PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 20-OCT-2000; 2000US-0241826P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
PR 08-NOV-2000; 2000US-0246527P.  
PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249264P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 17-NOV-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 05-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-483426/52.

P-PSDB; AAM88997.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides,  
useful for preventing, diagnosing and/or treating cancers and metastasis.

Claim 1; SEQ ID NO 6838; 3071pp + Sequence Listing; English.

XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)  
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic  
CC activity, and can be used in gene therapy and vaccine production. (I)  
CC proteins and polynucleotides may be used in the prevention, diagnosis and  
CC treatment of diseases associated with inappropriate (I) expression. For  
CC example, they may be used to treat disorders associated with decreased  
CC expression by rectifying mutations or deletions in a patient's genome  
CC that affect the activity of (I) by expressing inactive proteins or to  
CC supplement the patient's own production of (I). Additionally, (I)  
CC polynucleotides may be used to produce the secreted (I), by inserting the  
CC nucleic acids into a host cell and culturing the cell to express the  
CC protein. (I) proteins and polynucleotides may be used to prevent,  
CC diagnose and treat immune/haematopoietic-related diseases, especially  
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703  
CC to AAK87694 represent human immune/haematopoietic antigen genomic  
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169  
CC represent sequences used in the exemplification of the present invention  
XX  
SQ Sequence 689 BP; 138 A; 193 C; 207 G; 143 T; 0 U; 8 Other;  
  
Query Match 57.4%; Score 22.4; DB 4; Length 689;  
Best Local Similarity 81.2%; Pred. No. 1.3e+02;  
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
  
QY 1 TTGAGGACAGGACACTCCACAGCTCCCGCC 32  
DB 486 TTGAGGACATGCAGATCCACAGCTCTCGCC 455  
  
RESULT 14  
AA527743  
ID AAS27743 standard; DNA; 7667 BP.  
XX  
AC AAS27743;  
XX  
DT 07-NOV-2001 (first entry)  
DE  
DE DNA encoding novel signal transduction pathway protein, Seq ID 1403.  
XX Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;  
KW antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;  
KW immune system disorder; rheumatoid arthritis; inflammatory condition;  
KW organ transplant rejection; infection; hepatitis C; blood disorder;  
KW sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;  
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;  
KW chromosomal abnormality; Down syndrome; ischaemia; renal disorder;  
KW cardiovascular; respiratory; wound healing; endocrine; Addison's disease;  
KW reproductive system; gastrointestinal; liver disorder; AIDS; ds;  
KW acquired immune deficiency syndrome.  
XX Homo sapiens.  
XX  
XX WO200154733-A1.  
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XX 17-JAN-2001; 2001WO-US0001312.  
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PR 06-DEC-2000; 2000US-0251479P.  
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PR 08-DEC-2000; 2000US-0251989P.  
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(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-465460/50.

Novel polypeptides useful for diagnosing, treating, preventing and/or  
prognosing disorders related to the proteins, including cancers, immune  
disorders and neuronal disorders.

Claim 1; SEQ ID NO 1403; 880pp; English.

The invention relates to novel isolated polypeptides (I), and  
polynucleotides (II). (I), (II) and the antibody to (I) are useful for  
diagnosing, preventing and treating diseases including immune system  
disorders (e.g. congenital and acquired immunodeficiencies, autoimmune  
disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ  
transplant rejections and graft versus host disease, infectious diseases  
(e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and  
other blood-related disorders (sickle cell anaemia), myeloproliferative  
disorders, primary haematopoietic disorders, hyperproliferative disorders  
(e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g.  
Alzheimer's disease, Parkinson's disease), chromosomal abnormalities

CC (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g.  
glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),  
CC respiratory disorders, dermatological disorders, in wound healing,  
CC epithelial cell proliferation, endocrine disorders (e.g. Addison's  
disease), reproductive system disorders, gastrointestinal disorder  
CC (inflammatory disorders), liver disorders (cirrhosis), as stimulators of  
CC B-cell responsiveness to pathogens, activators of T-cells, to induce  
CC higher affinity antibodies, and as a means to induce tumour proliferation  
CC in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAS26976-  
CC AAS27850 represent novel signal transduction pathway protein coding  
CC sequences and PCR primers of the invention

SQ Sequence 7667 BP; 1717 A; 2370 C; 2150 G; 1430 T; 0 U; 0 Other;

Query Match 57.4%; Score 22.4; DB 4; Length 7667;

Best Local Similarity 81.2%; Pred. No. 1.7e+02;

Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TTGAGGACAGGACAGCTCCAGCTCCGCCC 32

DB 809 TTGGGACATGCAGAAATCCAGCTCTCGCC 840

RESULT 15

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ID AAK82163 standard; DNA; 7667 BP.

XX AAK82163;

DT 07-NOV-2001 (first entry)

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36975.

KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
cytostatic; gene therapy; vaccine; metastasis; ds.

OS Homo sapiens.

XX WO200157182-A2.

PD 09-AUG-2001.

XX 17-JAN-2001; 2001WO-US001354.

XX 31-JAN-2000; 2000US-0179065P.

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PR 08-NOV-2000; 2000US-0246528P.  
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XX (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Barash SC, Ruben SM;  
XX WPI; 2001-483426/52.

PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,  
XX useful for preventing, diagnosing and/or treating cancers and metastasis.

XX Disclosure; SEQ ID NO 36975; 3071pp + Sequence Listing; English.

XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)  
CC amino acid sequences given in AAK62170 to AAK61921. (I) have cytostatic  
CC activity, and can be used in gene therapy and vaccine production. (I)  
CC proteins and polynucleotides may be used in the prevention, diagnosis and  
CC treatment of diseases associated with inappropriate (I) expression. For  
CC example, they may be used to treat disorders associated with decreased  
CC expression by rectifying mutations or deletions in a patient's genome  
CC that affect the activity of (I) by expressing inactive proteins or to  
CC supplement the patient's own production of (I). Additionally, (I)  
CC polynucleotides may be used to produce the secreted (I), by inserting the  
CC nucleic acids into a host cell and culturing the cell to express the  
CC protein. (I) proteins and polynucleotides may be used to prevent,  
CC diagnose and treat immune/hematopoietic-related diseases, especially  
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703  
CC to AAK87694 represent human immune/hematopoietic antigen genomic  
CC sequences from the present invention. AAK54942 to AAK54950 and AAK62169  
CC represent sequences used in the exemplification of the present invention

XX Sequence 7667 BP; 1430 A; 2150 C; 2370 G; 1717 T; 0 U; 0 Other;

Query Match 57.4%; Score 22.4; DB 4; Length 7667;  
Best Local Similarity 81.2%; Pred. NO. 1.7e+02;  
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TTGAGGACAGGACATCCACAGCTCCGCC 32

Db 6859 TTGGGGACATGCAGATCCACAGCTCTCGCC 6828

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Job time : 27.9367 secs

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